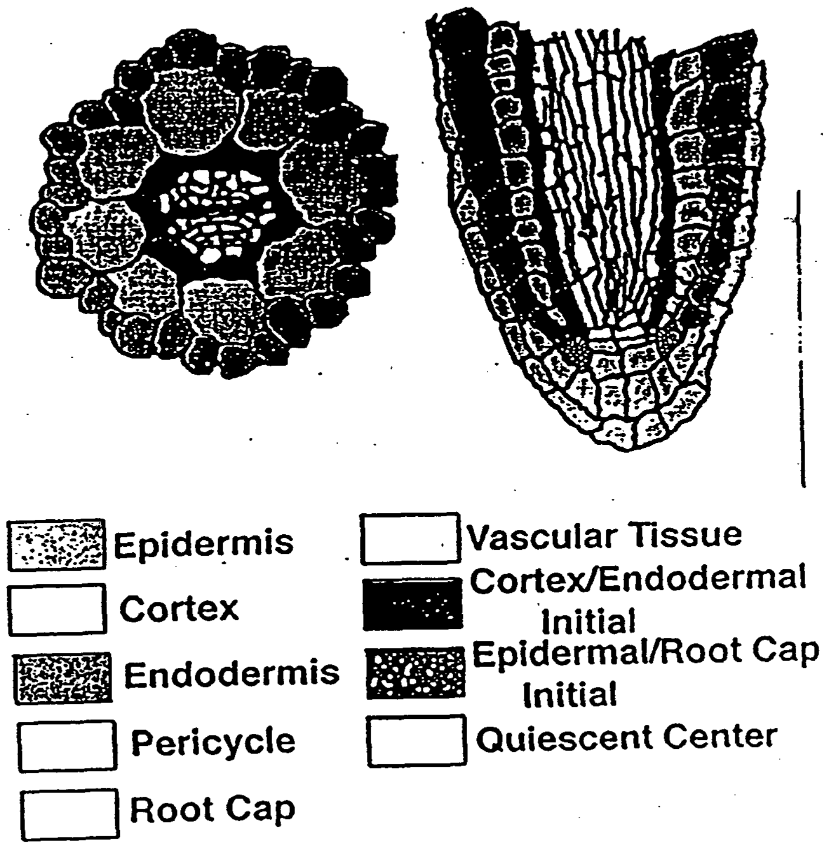

Epidermis
Cortex
Endodermis
Pericycle
Root Cap
Vascular Tissue
Cortex/Endodermal Initial
Epidermal/Root Cap Initial
Quiescent Center

FIG. 1A

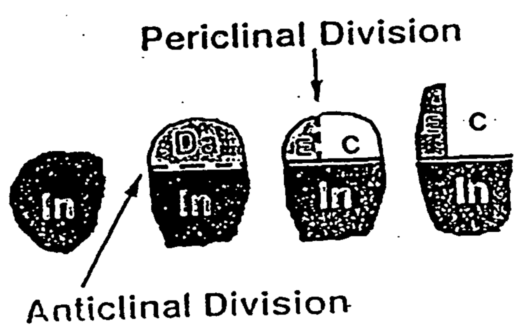

Periclinal Division
Da
E
C
C
In
In
In
In
Anticlinal Division

FIG. 1B

FIG. 2A

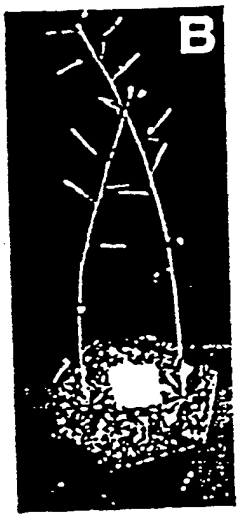


FIG. 2B

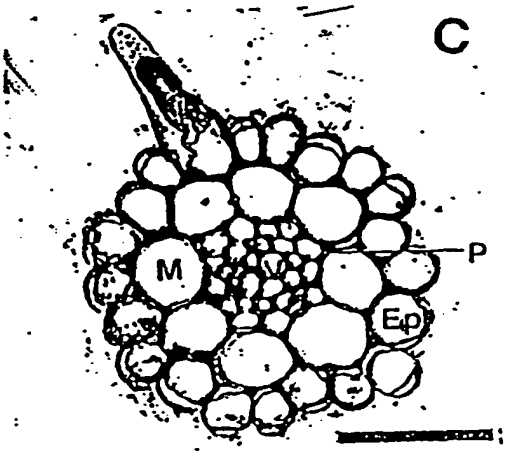


FIG. 2C

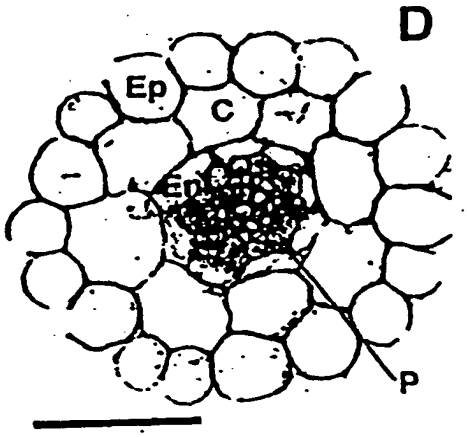


FIG. 2D

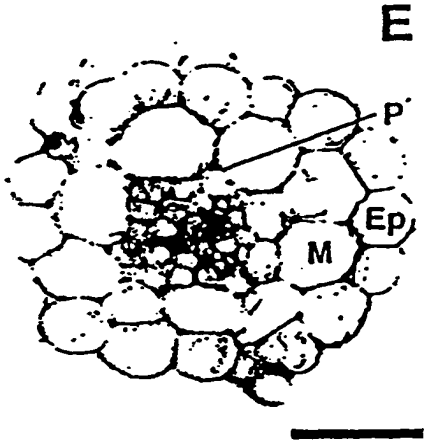


FIG: 2E

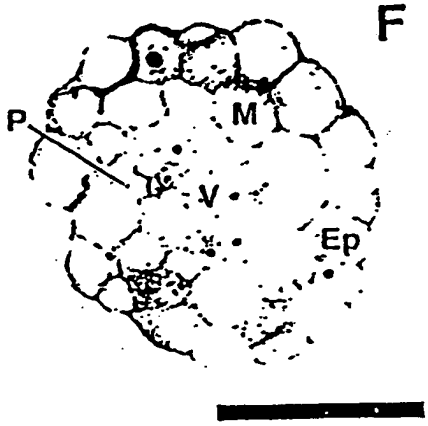


FIG. 2F

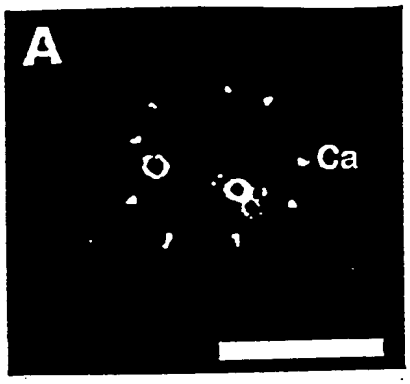


FIG. 3A

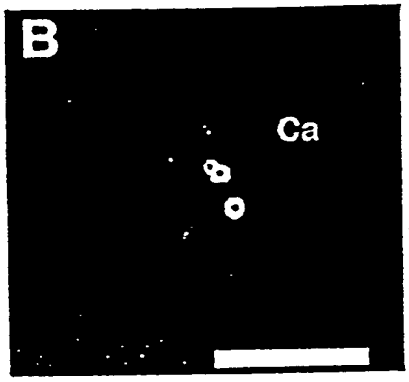


FIG. 3B

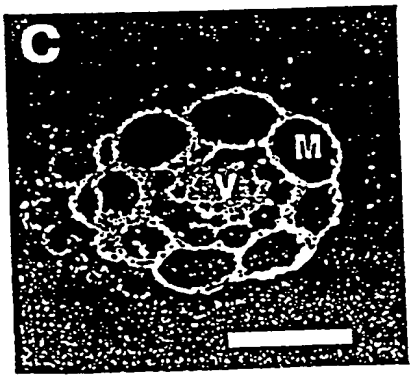


FIG. 3C

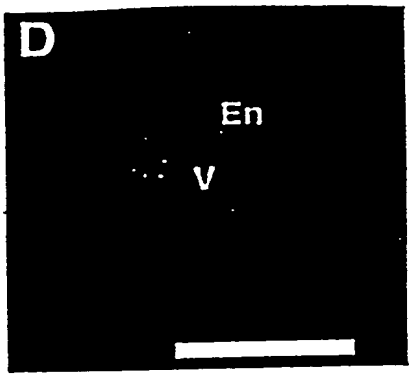


FIG. 3D

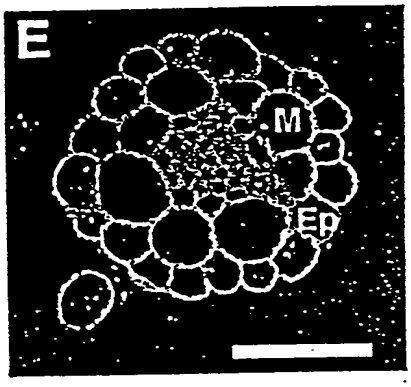


FIG. 3E

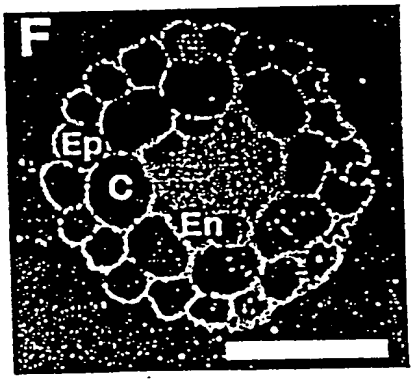


FIG. 3F

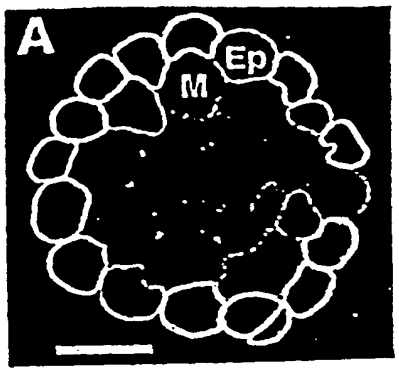


FIG. 4A

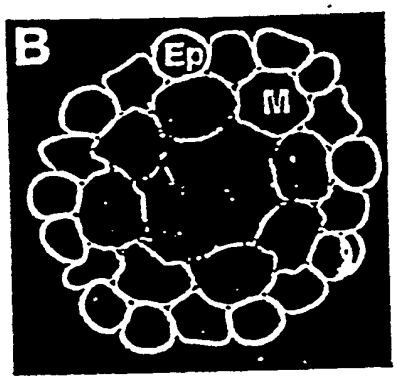


FIG. 4B

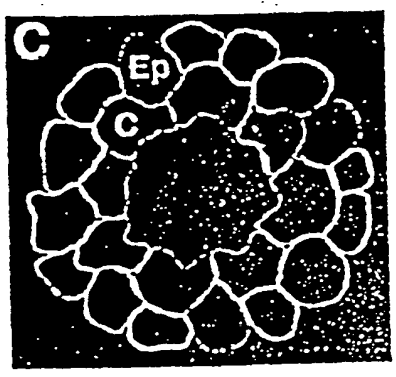


FIG. 4C

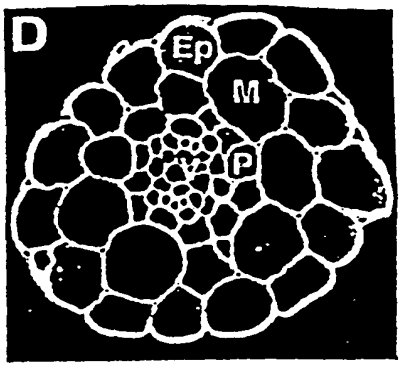


FIG. 4D

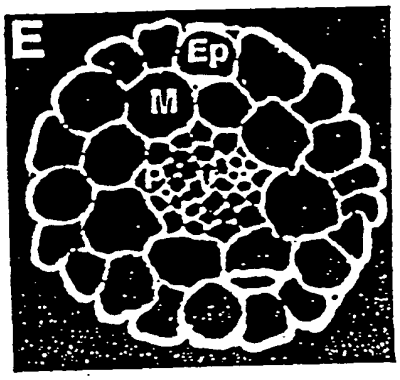


FIG. 4E

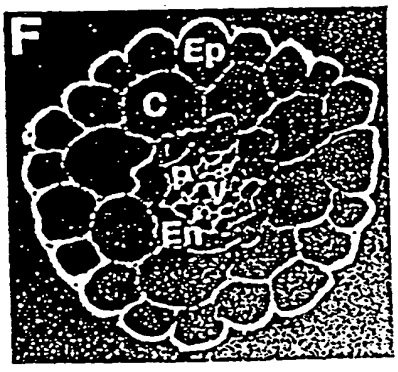


FIG. 4F

```
         10        20        30        40        50        60        70        80        90        100       110       120
      -41                                     +1
CCTTATTTATAACCATGCAATCTCACGACCAACAACCCTTCAATCTCCATGGCGGAATCCGGCGATTTCAACGGTGGTCAACCTCCTCCTCATAGTCCTCTGAGAATAATCTCTTCCGGT
                                                M  A  E  S  G  D  F  N  G  G  Q  P  P  P  H  S  P  L  R  I  I  S  S  G      24
AGTAGCAGCAGCAACAACCGTGGTCCTCCTCCTCCTCCTCCTCCTCCTTTAGTGATGGTGAGAAAAAGATTAGCTTCCGAGAATAGCTCTAACCCTGACTACAACAACTCCTCTCGTCCT
S  S  S  S  N  N  R  G  P  P  P  P  P  P  P  P  L  V  M  V  R  K  R  L  A  S  E  N  S  S  N  P  D  Y  N  N  S  S  R  P      64
CCTCGCCGTGTCTCTCACCTTCTTGACTCCAACTACAATATCGTCATACCACAACAACCACCGTCTCTTACCGCGGCGGCTACTGTATCTTCTCAACCAAACCCACCACTCTCTGTTTGT
P  R  R  V  S  H  L  L  D  S  N  Y  N  I  V  I  P  Q  Q  P  P  S  L  I  A  A  A  I  V  S  S  Q  P  N  P  P  L  S  V  C      104
GGCTTCTCTGGTCTTCCCGTTTTTCCTTCAGACCGTGGTGGTCGGAATGTTATGATGTCCGTACAACCAATGGATCAAGACTCTTCATCTTCTTCTGCTTCACCTACTGTATGGGTTGAC
G  F  S  G  L  P  V  F  P  S  D  R  G  G  R  N  V  M  M  S  V  Q  P  M  D  Q  D  S  S  S  S  S  A  S  P  T  V  W  V  D      144
GCCATTATCAGAGACCTTATCCATTCCTCAACTTCAGTCTCTATTCCTCAACTTATCCAAAACGTTAGAGACATTATCTTCCCTTGTAACCCAAATCTCGGTGCTCTTCTTGAATACAGG
A  I  I  R  D  L  I  H  S  S  T  S  V  S  I  P  Q  L  I  Q  N  V  R  D  I  I  F  P  C  N  P  N  L  G  A  L  L  E  Y  R      184
CTCCGATCTCTCATGCTCCTTGATCCTTCCTCTTCCTCTGACCCTTCTCCTCAAATCTTCGAACCTCTCTATCAGATCTCCAACAATCCTTCTCCTCCACAACAGCAACAGCAGCACCAA
L  R  S  L  M  L  L  D  P  S  S  S  S  D  P  S  P  Q  I  F  E  P  L  Y  Q  I  S  N  N  P  S  P  P  Q  Q  Q  Q  Q  H  Q      224
CAACAACAACAACAGCATAAGCCTCCTCCTCCTCCGATTCAGCAGCAAGAAAGAGAAAATTCTTCTACCGATGCACCACCGCAACCAGAGACAGTGATCGCCATCGTTCCCGCCGTCCAA
Q  Q  Q  Q  Q  H  K  P  P  P  P  P  I  Q  Q  Q  E  R  E  N  S  S  T  D  A  P  P  Q  P  E  T  V  I  A  I  V  P  A  V  Q      264
ACAAATACGGCGGAGGCTTTAAGAGAGAGGAAGGAAGAGATTAAGAGGCAGAAGCAAGACGAAGAAGGATTACACCTTCTCACATTGCTGCTACAGTGTGCTGAAGCTGTCTCTGCTGAT
T  N  T  A  E  A  L  R  E  R  K  E  E  I  K  R  Q  K  Q  D  E  E  G  L  H  L  L  T  L  L  L  Q  C  A  E  A  V  S  A  D      304
AATCTCGAAGAAGCAAACAAGCTTCTTCTTGAGATCTCTCAGTTATCAACTCCTTACGGGACCTCAGCGCAGAGAGTAGCTGCTTACTTCTCGGAAGCTATGTCAGCGAGATTACTCAAC
N  L  E  E  A  N  K  L  L  L  E  I  S  Q  L  S  T  P  Y  G  T  S  A  Q  R  V  A  A  Y  F  S  E  A  M  S  A  R  L  L  N      344
TCGTGTCTCGGAATTTACGCCGCCTTGCCTTCACGGCATCATCCTCAAACGCATAGCTTGAAAATGGTCTCTGCGTTTCAGGTCTTTAATGGGATAAGCCCTTTAGTGAAATTCTCACAC
S  C  L  G  I  Y  A  A  L  P  S  R  H  H  P  Q  T  H  S  L  K  M  V  S  A  F  Q  V  F  N  G  I  S  P  L  V  K  F  S  H      384
TTTACAGCCAATCAGGCCATTCAAGAAGCATTTGAGAAAGAAGACAGTGTACACATCATTGACTTGGACATCATGCAGGGACTTCAATGGCCTGGTTTATTCCACATTCTTGCTTCTAGA
F  T  A  N  Q  A  I  Q  E  A  F  E  K  E  D  S  V  H  I  I  D  L  D  I  M  Q  G  L  Q  W  P  G  L  F  H  I  L  A  S  R      424
CCTGGAGGACCTCCACACGTCCGACTCACGGGACTTGGTACTTCCATGGAAGCTCTTCAGGCTACAGGGAAACGTCTTTCGGATTTCACAGATAAGCTTGGCCTGCCTTTTGAGTTCTGC
P  G  G  P  P  H  V  R  L  T  G  L  G  T  S  M  E  A  L  Q  A  T  G  K  R  L  S  D  F  T  D  K  L  G  L  P  F  E  F  C      464
CCTTTAGCTGAGAAAGTTGGAAACTTGGACACTGAGAGACTCAATGTGAGGAAAAGGGAAGCTGTGGCTGTTCACTGGCTTCAACATTCTCTTTATGATGTCACTGGCTCTGATGCACAC
P  L  A  E  K  V  G  N  L  D  T  E  R  L  N  V  R  K  R  E  A  V  A  V  H  W  L  Q  H  S  L  Y  D  V  T  G  S  D  A  H      504
ACTCTCTGGTTACTCCAAAGGTAAAATAAACATTACCTTTTAATCACTCTTTATCTATAAATTATTTTAAGATTATATAGGAAAGATATGTTCTAAAAACCTGGCTTTTTTGGTTAATGA
T  L  W  L  L  Q  R                                                                                                          511
TTGGGGAATGAACAGATTAGCTCCTAAAGTTGTCACAGTAGTGGAGCAAGATTTGAGCCACGCTGGTTCTTTCTTAGGAAGATTTGTAGAGGCAATACATTACTACTCTGCACTCTTTGA
               L  A  P  K  V  V  T  V  V  E  Q  D  L  S  H  A  G  S  F  L  G  R  F  V  E  A  I  H  Y  Y  S  A  L  F  D      546
CTCACTGGGAGCAAGCTACGGCGAAGAGAGTGAAGAGAGACATGTCGTGGAACAGCAGCTATTATCGAAAGAGATACGGAATGTATTAGCCGTTGGAGGACCATCGAGAAGCGGTGAAGT
 S  L  G  A  S  Y  G  E  E  S  E  E  R  H  V  V  E  Q  Q  L  L  S  K  E  I  R  N  V  L  A  V  G  G  P  S  R  S  G  E  V     586
GAAGTTTGAGAGCTGGAGGGAGAAAATGCAACAATGTGGTTTTAAAGGTATATCTTTAGCTGGAAATGCAGCTACACAAGCGACTCTACTGTTGGGAATGTTTCCTTCGGATGGTTACAC
 K  F  E  S  W  R  E  K  M  Q  Q  C  G  F  K  G  I  S  L  A  G  N  A  A  T  Q  A  T  L  L  L  G  M  F  P  S  D  G  Y  T     626
TTTGGTTGATGATAATGGTACACTTAAGCTTGGATGGAAAGATCTTTCGTTACTCACTGCTTCAGCTTGGACGCCTCGTTCTTAGTTTTCTTCTCCTTTTTCACAAACAATGTCCCCATA
 L  V  D  D  N  G  T  L  K  L  G  W  K  D  L  S  L  L  T  A  S  A  W  T  P  R  S  STOP                                        653
2163
AAT
```

FIG. 5A

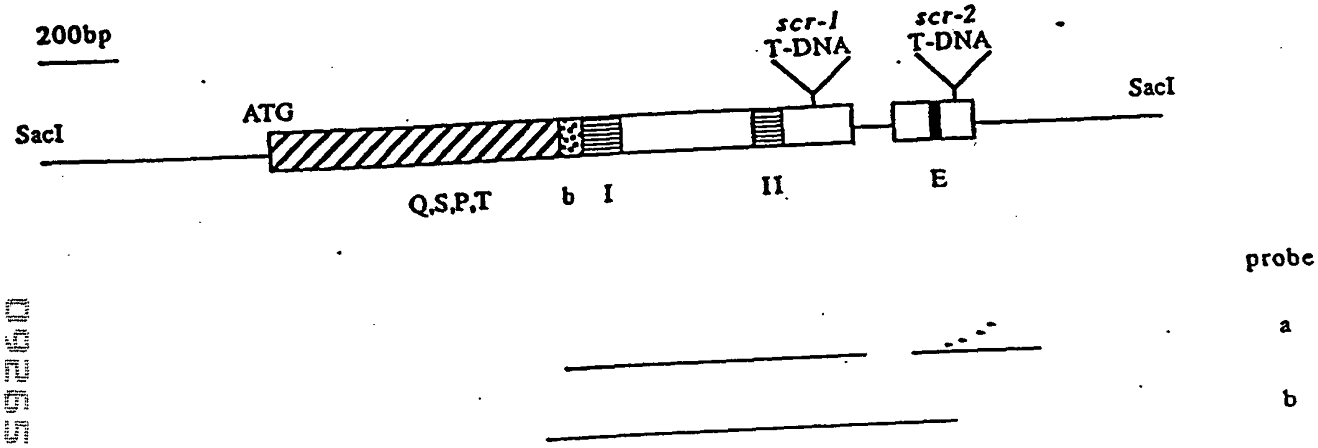


FIG. 5B

```
                                                                1
SCR bZIP-like domain                PAVQTNTAEALRERKEEIKRQKQ     D
                                         ||  | | |   : | ||

GCN4        (yeast)                 LKRARNTEAARRSRARKLQRMKQ     L
TGA1        (Arabidopsis)           RRLAQNREAARKSRLRKKAYVQQ     L
C-Fos       (mouse)                 IRRERNKMAAAKCRNRRRELTDT     L
c-JUN       (human)                 RKRMRNRIAASKCRKRKLERIAR     L
CREB        (human)                 VRLMKNREAARECRRKKKEYVKC     L
Opaque-2    (maize)                 KRKESNRESARRSRYRKAAHLKE     L
OBF2        (maize)                 MRQIRNRDSAMKSRERKKSYIKD     L
RAF-1       (rice)                  RRMVSNRESARRSRKKKQAHLAD     L
```

FIG. 5C

SCR VHIID domain 1

SCR AFEKEDSVHIIDLDIMQGLQWPGLFHILASRPGGPPHVRLTGL

F13896 AVKNESFVHIIDFQISQGGQWVSLIRALGARPGGPPNVRITGI

Z37192 AMEGEKMVHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGV

Z25645 AIKGEEEVHIIDFDINQGNQYMTLIRSIA

D41474 IHVIDFXLGVGGQWASFLQELAHRRG

T18310 VHIIXFXLMQGLQWPALMDVFSARKGGPPKLRITGI

FIG. 5D

MetAlaGluSerGlyAspPheAsnGlyGlyGlnProProProHisSerProLeuArgThr
ThrSerSerGlySerSerSerSerAsnAsnArgGlyProProProProProProPr Pro
LeuValMetValArgLysArgLeuAlaSerGluMetSerSerAsnProAspTyrAsnAsn
SerSerArgProProArgArgValSerHisLeuLeuAspSerAsnTyrAsnThrValThr
ProGlnGlnProProSerLeuThrAlaAlaAlaThrValSerSerGlnProAsnProPro
LeuSerValCysGlyPheSerGlyLeuProValPheProSerAspArgGlyGlyArgAsn
ValMetMetSerValGlnProMetAspGlnAspSerSerSerSerSerAlaSerProThr
ValTrpValAspAlaIleIleArgAspLeuIleHisSerSerThrSerValSerIlePro
GlnLeuIleGlnAsnValArgAspIleIleProCysAsnProAsnLeuGlyAlaLeu
LeuGluTyrArgLeuArgSerLeuMetLeuLeuAspProSerSerSerSerAspProSer
ProGlnThrPheGluProLeuTyrGlnIleSerAsnAsnProSerProProGlnGlnGln
GlnGlnHisGlnGlnGlnGlnGlnGlnHisLysProProProProProIleGlnGlnGln
GluArgGluAsnSerSerThrAspAlaProProGlnProGluThrValThrAlaThrVal
ProAlaValGlnThrAsnThrAlaGluAlaLeuArgGluArgLysGluGluIleLysArg
GlnLysGlnAspGluGluGlyLeuHisLeuLeuThrLeuLeuLeuGlnCysAlaGluAla
ValSerAlaAspAsnLeuGluGluAlaAsnLysLeuLeuLeuGluIleSerGlnLeuSer
ThrProTyrGlyThrSerAlaGlnArgValAlaAlaTyrPheSerGluAlaMetSerAla
ArgLeuLeuAsnSerCysLeuGlyIleTyrAlaAlaLeuProSerArgTrpMetProGln
ThrHisSerLeuLysMetValSerAlaPheGlnValPheAsnGlyIleSerProLeuVal
LysPheSerHisPheThrAlaAsnGlnAlaIleGlnGluAlaPheGluLysGluAspSer
ValHisIleIleAspLeuAspIleMetGlnGlyLeuGlnTrpProGlyLeuPheHisIle
LeuAlaSerArgProGlyGlyProProHisValArgLeuThrGlyLeuGlyThrSerMet
GluAlaLeuGlnAlaThrGlyLysArgLeuSerAspPheThrAspLysLeuGlyLeuPro
PheGluPheCysProLeuAlaGluLysValGlyAsnLeuAspThrGluArgLeuAsnVal
ArgLysArgGluAlaValAlaValHisTrpLeuGlnHisSerLeuTyrAspValThrGly
SerAspAlaHisThrLeuTrpLeuLeuGlnArgLeuAlaProLysValValThrValVal
GluGlnAspLeuSerHisAlaGlySerPheLeuGlyArgPheValGluAlaIleHisTyr
TyrSerAlaLeuPheAspSerLeuGlyAlaSerTyrGlyGluGluSerGluGluArgHis
ValValGluGlnGlnLeuLeuSerLysGluIleArgAsnValLeuAlaValGlyGlyPro
SerArgSerGlyGluValLysPheGluSerTrpArgGluLysMetGlnGlnCysGlyPhe
LysGlyIleSerLeuAlaGlyAsnAlaAlaThrGlnAlaThrLeuLeuLeuGlyMetPhe
ProSerAspGlyTyrThrLeuValAspAspAsnGlyThrLeuLysLeuGlyTrpLysAsp
LeuSerLeuLeuThrAlaSerAlaTrpThrProArgSerSTOP

FIG. 5E

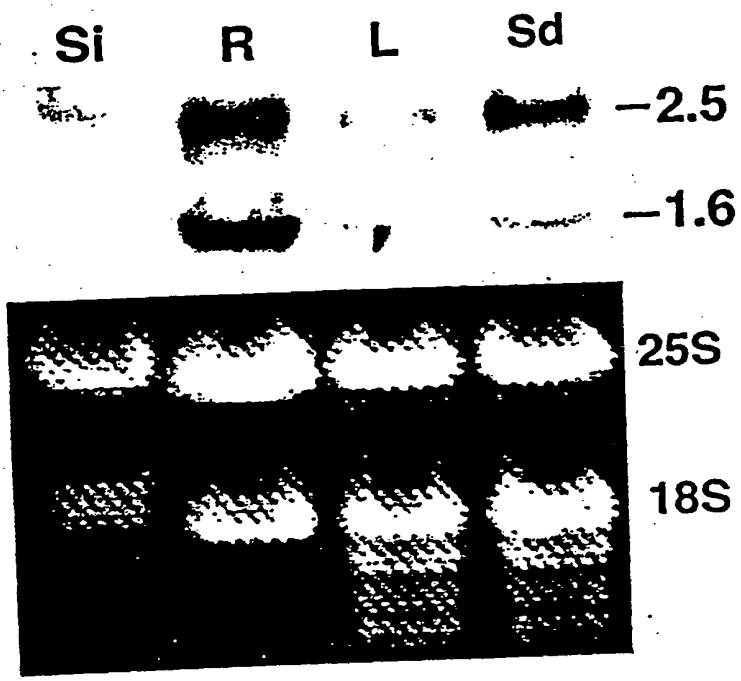


FIG. 6A

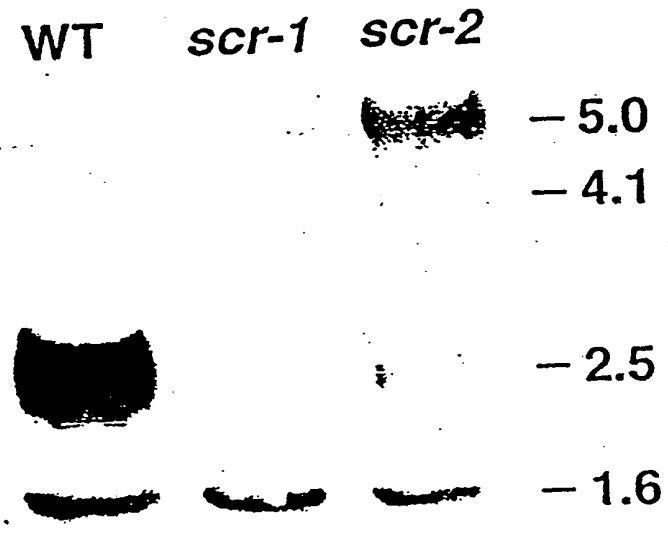


FIG. 6B

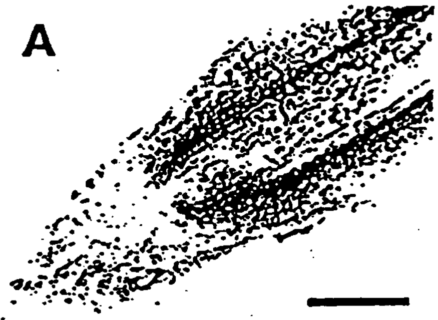


FIG. 7A

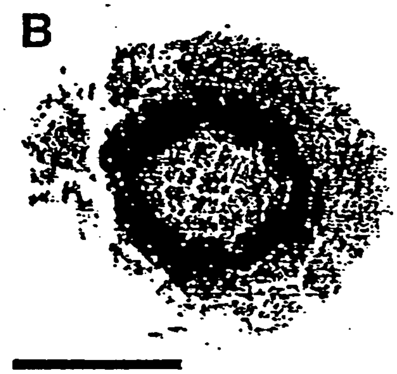


FIG. 7B

FIG. 7C

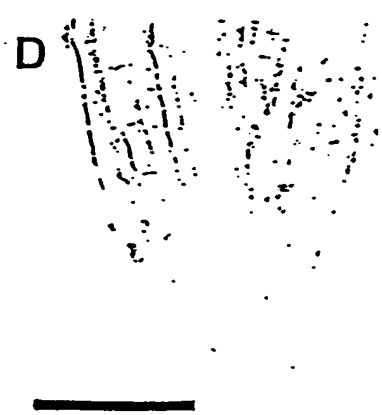


FIG. 7D

FIG. 7E

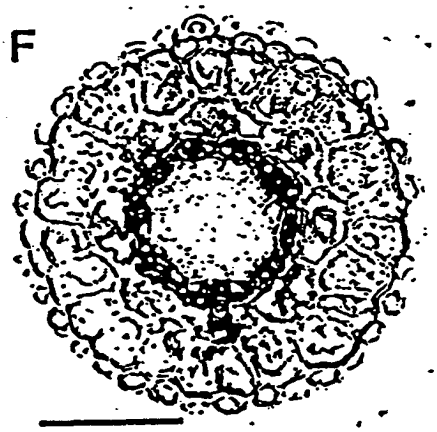


FIG. 7F

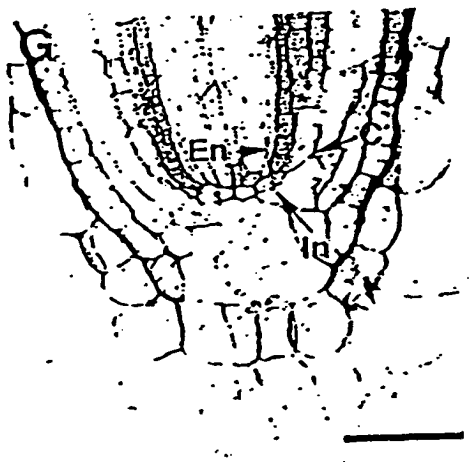


FIG. 7G

```
        10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GGCACGAGCC CAACGGGTCC TGAGCTTCTT ACTTATATGC ATATCTTGTA   50
G  T  S  P   T  G  P   E  L  L   T  Y  M  H   I  L  Y

TGAAGCCTGC CCTTATTTCA AATTCGGTTA TGAATCTGCT AATGGAGCTA   100
 E  A  C   P  Y  F  K   F  G  Y   E  S  A   N  G  A  I

TAGCTGAAGC TGTGAAGAAC GAAAGTTTTG TGCACATTAT CGATTTCCAG   150
  A  E  A   V  K  N   E  S  F  V   H  I  I   D  F  Q

ATTTCTCAAG GTGGTCAATG GGTGAGTTTG ATCCGTGCTC TTGGTGCTAG   200
I  S  Q  G   G  Q  W   V  S  L   I  R  A  L   G  A  R

ACCTGGTGGA CCTCCGAACG TTAGGATAAC GGGAATTGAT GATCCGAGAT   250
 P  G  G   P  P  N  V   R  I  T   G  I  D   D  P  R  S

CATCGTTTGC TCGTCAAGGA GGACTTGAGT TAGTTGGACA AAGACTTGGG   300
 S  F  A   R  Q  G   G  L  E  L   V  G  Q   R  L  G

AAGCTAGCTG AAATGTGCGG TGTTCCGTTT GAGTTCCATG GAGCTGCTTT   350
K  L  A  E   M  C  G   V  P  F   E  F  H  G   A  A  L

ATGCTGCACG GAAGTCGAAA TCGAGAAGCT AGGAGTTAGA AATGGAGAAG   400
 C  C  T   E  V  E  I   E  K  L   G  V  R   N  G  E  A

CGCTCGCGGT TAACTTCCCG CTTGTTCTTC ACCACATGCC TGATGAGAGT   450
 L  A  V   N  F  P   L  V  L  H   H  M  P   D  E  S

GTAACTGTGG AGAATCACAG AGATAGATTG TTGAGATTGG TCAAACACTT   500
V  T  V  E   N  H  R   D  R  L   L  R  L  V   K  H  L

GTCACCAAAC GTTGTGACTC TGGTTGAGCA AGAAGCGAAT ACAAACACTG   550
 S  P  N   V  V  T  L   V  E  Q   E  A  N   T  N  T  A

CGCCGTTTCT TCCCCGGTTT GTCGAGACAA TGAACCATTA CTTGGCAGTT   600
 P  F  L   P  R  F   V  E  T  M   N  H  Y   L  A  V
```

FIG. 8

```
        10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
TTCGAATCAA TAGATGTGAA ACTCGCTAGA GATCACAAGG AAAGGATCAA      650
F  E  S  I  D  V  K  L  A  R  D  H  K  E  R  I  N

TGTTGAGCAG CATTGTTTGG CTAGAGAGGT TGTGAATCTT ATAGCTTGTG      700
 V  E  Q  H  C  L  A  R  E  V  V  N  L  I  A  C  E

AAGGTGTTGA AAGAGAAGAG AGGCACGAGC CACTAGGGAA ATGGAGGTCT      750
  G  V  E  R  E  E  R  H  E  P  L  G  K  W  R  S

CGGTTTCACA TGGCGGGATT TAAACCGTAT CCTTTGAGCT CGTATGTGAA      800
R  F  H  M  A  G  F  K  P  Y  P  L  S  S  Y  V  N

CGCAACAATC AAAGGATTGC TTGAGAGTTA TTCAGAGAAG TATACACTTG      850
 A  T  I  K  G  L  L  E  S  Y  S  E  K  Y  T  L  E

AAGAAAGAGA TGGAGCATTG TATTTAGGAT GGAAGAATCA ACCTCTTATC      900
  E  R  D  G  A  L  Y  L  G  W  K  N  Q  P  L  I

ACTTCTTGTG CTTGGAGGTA ACTAATAAAA ACCTTGTTCG GTTTCAGAAG      950
T  S  C  A  W  R  X

AGATTAGAAA CTTCTTTTAA AGTTTGCAGA ATCTGTTTGT AAAAGTAAAA     1000

CTCATGCATG ATCCGNAGGA ACAAGTTGTC AAATGTTGTA GTAGTAAGTG     1050

ATATGTTGAT GACCCAAAAA AAAAAAAAAA AAAAA                      1085
```

FIG. 8 (cont'd.)

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GCTATGGAAG GAGAGAAGAT GGTTCATGTG ATTGATCTCG ATGCTTCTGA      50
A M E G   E K M   V H V   I D L D   A S E

GCCAGCTCAA TGGCTTGCTT TGCTTCAAGC TTTTAACTCT AGGCCTGAAG     100
 P A Q  W L A L  L Q A  F N S  R P E G

GTCCACCTCA TTTGAGAATC ACTGGTGTTC ATCACCAGAA GGAAGTGCTT     150
 P P H  L R I  T G V H  H Q K  E V L

GAACAAATGG CTCATAGACT CATTGAGGAA GCAGAGAAAC TCGATATCCC     200
E Q M A  H R L  I E E  A E K L  D I P

GTTTCAGTTT AATCCCGTTG TGAGTAGGTT AGACTGTTTA AATGTAGAAC     250
 F Q F  N P V V  S R L  D C L  N V E Q

AGTTGCGGGT TAAAACAGGA GAGGCCTTAG CCGTTAGCTC GGTTCTTCAA     300
  L R V  K T G  E A L A  V S S  V L Q

TTGCATACCT TCTTGGCCTC TGATGATGAT CTCATGAGAA AGAACTGCGC     350
L H T F  L A S  D D D  L M R K  N C A

TTTACGGTTT CAGAACAACC CTAGTGGAGT TGACTTGCAG AGAGTTCTAA     400
 L R F  Q N N P  S G V  D L Q  R V L M

TGATGAGCCA TGGCTCTGCA GCTGAGGCAC GTGAGAATGA TATGAGTAAC     450
  M S H  G S A  A E A R  E N D  M S N

AACAATGGGT ATAGCCCTAG CGGTGACTCG GCCTCATCTT TGCCTTTACC     500
N N G Y  S P S  G D S  A S S  L P L P

AAGTTCAGGA AGGACTGATA GCTTCCTCAA TGCTATTTGG GGTTTGTCTC     550
 S S G  R T D S  F L N  A I W  G L S P

CAAAGGTCAT GGTGGTCACT GAGCAAGACT CAGACCACAA CGGCTCCACA     600
  K V M  V V T  E Q D  S D H  N G S T
```

FIG. 9

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
CTAATGGAGA GGCTATTAGA ATCACTTTAC ACCTACGCAG CATTGTTTGA      650
L M E R L L E S L Y T Y A A L F D

TTGCTTGGAA ACAAAAGTTC CAAGAACGTC TCAAGATAGG ATCAAAGTGG      700
 C L E T K V P R T S Q D R I K V E

AGAAGATGCT CTTCGGGGAG GAGATCAAGA ACATCATATC CTGCGAGGGA      750
  K M L F G E E I K N I I S C E G

TTTGAGAGAA GAGAAAGACA CGAGAAGCTT GAGAAATGGA GCCAGAGGAT      800
F E R R E R H E K L E K W S Q R I

CGATTTGGCT GGTTTTGGGA ATGTTCCTCT TAGCTATTAT GCGATGTTGC      850
 D L A G F G N V P L S Y Y A M L Q

AGGCTAGGAG ATTGCTTCAA GGGTGCGGTT TTGATGGGTA TAGAATCAAG      900
  A R R L L Q G C G F D G Y R I K

GAAGAGAGCG GGTGCGCAGT AATTTGCTGG CAAGATCGAC CTCTATACTC      950
E E S G C A V I C W Q D R P L Y S

GGTATCAGCT TGGAGATGCA GGAAGTGAAT GATATATTAC AGTTTGTCTT     1000
 V S A W R C R K X

CTATTTTGGT TATGAGCAGA GTCCCTTTCT TTTTTGTATA CATGGGGACA     1050

CAATCTTAGT TGTTTTGTGA TGGTGACTTT CTGTCTCTTT ATGCTATTTT     1100

GGCTTAAATG CTTCTACTGC CTCTGCATGT AAAGCCTTTG TGTGTTGGTT     1150

CAATTTGGTC TGGTGTGGGT GTAATACCAA ACCAAATCCA ATTTGAGCTG     1200

AAGATAACTA ATTTGATGAT CGGCTCGTGC C                         1231
```

FIG. 9 (cont'd.)

CTTTGTCAAT GGTAAATGAG CTGAGGCAGA TAGTTTCTAT CCAAGGAGAC 50
CCTTCTCAGA GAATCGCAGC TTACATGGTG GAAGGTCTAG CTGCAAGAAT 100
GGCCGCTTCA GGAAAATTCA TCTACAGAGC ATTGAAATGC AAAGAGCCTC 150
CTTCGGATGA GAGGCTTGCA GCTATGCAAG TCCTGTTTGA AGTCTGCCCT 200
TGTTTCAAGT TCGGGTTTTT AGCAGCTAAT GGTGCGATAC TTGAAGCAAT 250
CAAAGGTGAA GAAGAAGTTC ACATAATCGA TTTCGATATA AACCAAGGGA 300
ACCAATACAT GACACTGATA CGAAGCATTG CTGAGTTGCC TGGTAAACGA 350
CCTCGCCTGA GGTTAACAGG AATTGATGAC CCTGAATCAG TCCAACGCTC 400
CATTGGAGGG CTAAGAATCA TCAATCTAAG ACTCGAGCAA CTCGCAGAGG 450
ATAATGGAGT ATCCTTCAAA TTCAAAGCAA TGCCTTCAAA GACTTCGATT 500
GTCTCTCCAT CAACACTCGG TTGCAAACCA GGAGAAACCT TAATCAGTGA 550
ACTTTGCATT CCAACTTCAC CACATGCCTG ACGAGAGTGT CACAACAGTA 600
AACCAGCGGG ACGAGCTACT TCACATGGTC AAAAGCTTAA ACCCGCTTGT 650
CACGGTCGTT GAACAAGACG TGAACACAAA CACTTCACCG TTCTTTCCCA 700
GATTCATAGA GGCTTACGAA TACTACTCAG CAGTTTTCGA GTCTCTAGAC 750
ATGACACTTC CAAGAGAAAG CCAAGAGAGG ATGAATGTAG AAAGACAGTG 800
TCTCGCTAGA GACATAGTCA ACATTGTTGC TTGCGAAGGA GAAGAACGGA 850
TAGAGAGATA CGAGGCTGCG GGAAAATGGA GAGCAAGGAT GATGATGGCT 900
GGATTCAATC CAAAACCAAT GAGTGCTAAA GTAACCAACA ATATACAAAA 950
CCTGATAAAG CAACAATATT GCAATAAGTA CAAGCTTAAA GAAGAAATGG 1000
GTGAGCTCCA TTTTTGCTGG GAGGAGAAAA GCTTAATCGT TGCTTCAGCT 1050
TGGAGGTAAG ATAAGTGACA AGAGCATATA GTCTTTATGT TTCATAAAAC 1100
ATAATTATGT TTTTACTGTA ATCTTGGGTT ATTGTGTAAC TGGTTAAATC 1150
ATCTCCATGT ATTATTACCA GAGGTTAGGG GTGATCACAG GTACTAAAAG 1200
CTAATCTAAC ACTTATGGAA GAATTTTTCT TTCTTTTTTT TCCCTATTAT 1250
ATAAAAATAA TTAGAGTTTT GGTTCTAAAC CTATTTGCTA AGTGTGAATG 1300
AGTCTTTACA TGTTCATATT TCAGTTCAAA TGGTTAAATT TGTTAAGGTT 1350
CTCACTTAAA AAAAAA

FIG. 10

Zm-scl1

```
                10        20        30        40        50
CCAGGAGGCGTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACA
 Q  E  A  F  E  R  E  E  R  V  H  I  I  D  L  D  I

                60        70        80        90       100
TCATGCAGGGGCTGCAGTGGCCGGGCCTCTTCCACATCCTTGCCTCCCGC
   M  Q  G  L  Q  W  P  G  L  F  H  I  L  A  S  R
```

FIG. 11 A

```
           10         20         30         40         50
  1234567890 1234567890 1234567890 1234567890 1234567890
CCACGCGTCCG TCAAAGGATA CAACCATGTA CACATAATTG ACTTTTCCCT   50
 H  A  S  V   K  G  Y   N  H  V   H  I  I  D   F  S  L

GATGCAAGGT CTCCAGTGGC CGGCACTCAT GGATGTCTTC TCCGCCCGTG   100
 M  Q  G   L  Q  W  P   A  L  M   D  V  F   S  A  R  E

AGGGTGGGCC ACCAAAGCTC CGAATCACAG GCATTGGCCC GAACCCAATA   150
  G  G  P   P  K  L   R  I  T  G   I  G  P   N  P  I

GGTGGCCGTG ACGAGCTCCA TGAAGTGGGA ATTCGCCTCG CCAAGTATGC   200
 G  G  R  D   E  L  H   E  V  G   I  R  L  A   K  Y  A

ACACTCGGTG GGTATCGACT TCACTTTCCA GGGAGTCTGT GTCGATCAAC   250
  H  S  V   G  I  D  F   T  F  Q   G  V  C   V  D  Q  L

TTGATAGGTT GTGCGACTGG ATGCTTCTCA AACCAATCAA AGGAGAGGCA   300
  D  R  L   C  D  W   M  L  L  K   P  I  K   G  E  A

GTTGCCATAA ACTCCATCCT ACAACTCCAT CGCCTCCTCG TTGACCCAGA   350
 V  A  I  N   S  I  L   Q  L  H   R  L  L  V   D  P  D

TGCAAACCCA GTGGTGCCCG CACCAATAGA TATCCTCCTC AAATTGGTCA   400
  A  N  P   V  V  P  A   P  I  D   I  L  L   K  L  V  I

TCAAGATAAA CCCCATGATC TTCACGGTGG TTGAGCATGA GGCAGATCAC   450
  K  I  N   P  M  I   F  T  V  V   E  H  E   A  D  H

AACAGACCAC CACTACTAGA GAGGTTCACT AATGCCCTCT TCCACTATGC   500
 N  R  P  P   L  L  E   R  F  T   N  A  L  F   H  Y  A

GACCATGTTT GACTCTTTGG AGGCCATGCA TCGTTGTACC AGTGGTAGAG   550
  T  M  F   D  S  L  E   A  M  H   R  C  T   S  G  R  D

ACATCACCGA CTCACTCACA GAGGTGTACC TTCGAGGTGA GATTTTTGAC   600
  I  T  D   S  L  T   E  V  Y  L   R  G  E   I  F  D
```

FIG. 11B

```
           10          20          30          40          50
1234567890 1234567890 1234567890 1234567890 1234567890
ATTGTCTGCG GCGAGGGCAG TGCACGCACC GAACGTCATG AGTTGTTTGG     650
 I  V  C  G   E  G  S   A  R  T   E  R  H  E   L  F  G

TCACTGGAGG GAGAGGCTCA CCTATGCTGG GCTAACTCAA GTGTGGTTCG     700
 H  W  R   E  R  L  T   Y  A  G   L  T  Q   V  W  F  D

ACCCCGATGA GGTTGACACG CTAAAAGACC AGTTGATCCA TGTGACATCC     750
  P  D  E   V  D  T   L  K  D  Q   L  I  H   V  T  S

TTATCTGGCT CTGGGTTCAA CATCCTAGTG TGTGATGGCA GCCTTGCACT     800
 L  S  G  S   G  F  N   I  L  V   C  D  G  S   L  A  L

AGCGTGGCAT AATCGCCCGT TATATGTGGC AACAGCTTGG TGTGTGACAG     850
 A  W  H   N  R  P  L   Y  V  A   T  A  W   C  V  T  G

GAGGAAATGC TGCCAGTTCC ATGGTTGGCA ACATCTGTAA GGGTACAAAT     900
  G  N  A   A  S  S   M  V  G  N   I  C  K   G  T  N

GATAGTAGAA GAAAGGAAAA CCGTAATGGA CCCATGGAGT AGCAGGAAGA     950
 D  S  R  R   K  E  N   R  N  G   P  M  E  X

ATAACCATGT CATGAGCAAA TCGATCAAGT AATAAAATGC ACTGATGACA    1000

TGCATGGTGA TCTAAAGTTT TTTTGCGTGA ATGTGCAATG ACGAATTGTT    1050

CAATTTGAAT AACCTAATCA TGAGACTCAA AAAAAAAAAA AAA           1093
```

FIG. 11B(cont'd.)

CCCAACTTGG GAAGCCCTTC CTCCGCTCCG CCTCCTACCT CAAGGAGGCC 50
CTCCTCCTCG CACTCGCCGA CAGCCACCAT GGCTCCTCCG GCGTCACCTC 100
GCCGCTCGAC GTTGCCCTCA AGCTTGCAGC ATACAAGTCT TTCTCTGACC 150
TGTCACCTGT GCTCCAGTTC ACTAACTTTA CCGCAACAAG GCGCTTCTTG 200
ATGAGATTGG TGGCATGGCA ACTTCCTGCA TCCATGTCAT TGACTTTGAT 250
CTCGGTGTTG GTGGTCAGTG GGCTTCCTTC TTGCAGGAGC TTGCCCACCG 300
CCGGGGAGCT GGAGGTATGG CCTTGCCGTT GTTGAAGCTC ACGGCTTTCA 350
TGTCGACTGC TTCTCACCAT CCACTGGAGC TGCACCTTAC CCAGGATAAC 400
CTCTCTCAGT TTGCCGCAGA GCTCAGAATT CCTTTCGAAT TCAATGCCGT 450
CAGTCTTGAT GCATTCAATC CTGCGGAATC TATTTCTTCC TCTGGTGATG 500
AAGTTGTTGC TGTTAGCCTC CCTGTTGGCT GCTCTGCTCG TGCACCACCG 550
CTGCCAGCGA TTCTTCGGTT GGTGAAACAG CTTTGTCCTA AGGTTGTCGT 600
GGCTATTGAT C

FIG. 12A

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TACAGAGCAA CAGCAGTATA      50
ATATTAATTC TGTACCACAC AACCATTTGA TAGGTTAAAT TACCCTCTAG     100
TCTCTACTCA TAAGCAGTGT TTCCAATGAG ATGATCATGG CTAATTGAGC     150
AGAGCATGGC AACAACCTAA AGCAACATCA TTAGCTATAG AGACTGACAC     200
CAATATTCCT AAATCCACTA GGCTAGCTAA TAAGCTGCAA CGAAAAGCAA     250
TATGAAGAGT TCAACAGCTC AAGACAACAA TTTCATTTGC AACATTTAAT     300
TGCAAGAATA AATGGACATT ACTGGAGTGG TCGATGCTTG CAAACGGTGG     350
TGGAACCTTG GTGGAGTGAA GCTTATGGCT GATCAGCACC GCCAAGATGA     400
TATGGATACA AGCTCCCCAC GCTGCCAGTA GAGCGTAAGA GCAGCTCCGC     450
GTTTCTCCAC ATGGAATCCT CGGACCTGCA CCCGCTTCAG GAGGCAGTCT     500
GC
```

FIG. 12B

FIG. 13A

```
SCR     MAESGDFNGGQPPPHSPLRTTSSGSSSSNNRGPPPPPPPPLVMVRKR----LASEMSS
TF1     MKRD---HHQFQGRLSNHGTSSSSSSISKDK--MMMVKKEEDGGGNMDDELLAV----
TF4     MKRDHHHHHQ----------------------DKKTMMM--NEEDDGNGM-DELLAV----

                |-------------- MOTIF  I --------------|
SCR     NPDYNNSSRPPRRVSHLLDSNYNTVTPQQPPSLTAAATVSSQPNPPLSVCGFSG
TF1     -LGYKVRSSEMAEVALKLEQLETMMSNAQEDGLSHLATDAAHYNPSELYS----
TF4     -LGYKVRSSEMADVAQKLEQLEVMMSNVQEDDLSQLATETVHYNPAELYT----

SCR     LPVFPSDRGGRNVMMSVQPMDQDSSSSSASPTVWVDAIIRDLIHS----STSVSIPQL
TF1     ------------------------------------WLDNMLSELNPPPLPASSNGLDPVL
TF4     ------------------------------------WLDSMLTDLNPP----SSN-AEYDL

SCR     IQNVRDIIFPCNPNLGALLEYRLRSLMLLDPSSSSDPSPQTFEPLYQISNNPSP
TF1     PSPEICGFPXSDYDLKVIPXNAIYQFPAIDSSSSSNN--Q--------------
TF4     -----KAI-P---------GDILNQF-AIDSASSSN---Q--------------
```

FIG. 13B

```
                                                                    |-----
SCR       PQQQQQHQQQQQQHKPPPPPIQQQERENSSTDAPPQPETVTATVPAVQTNTAEA
TF1       ----------NKRLKSCSSPDSMVTSTSTGTQIGGVIGTTVTTTTTTTTAAAES
TF4       -------------------------GGGGDTYTTNKRLKCSNGVVETTTATAES


          -------- MOTIF II (DIMERIZATION?) ----------------
SCR       LRERKEEIKRQKQDEEGLHLLTLLLQCAEAVSADNLEEANKLLLEISQLSTPYG
1110                                                LSMVNELRQIVSIQG
TF1       ----TRSVILVDSQENGVRLVHALMACAEAIQQNNLTLAEALVKQIGCLAVSQA
TF4       ----TRHVVLVDSQENGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQI
3898                                                          QLGKPFL


          ----------------|                                   |-----
SCR       TSAQRVAAYFSEAMSARLLNSCLGIYAALPSRWMPQTHSLKMVSAFQVFNGISP
4818                                          GTSPT-GPELLTYMHILYEACP
1110      DPSQRIAAYMVEGLAARMAASGKFIYRAL-KCKEPPS--DERLAAMQVLFEVCP
TF1       GAMRKVATYFAEALARR-------IY-RL-SPPQNQIDHCLSDTLQMHFYETCP
TF4       GAMRQVATYFAEALARR-------IY-RL-SPSQSPIDHSLSDTLQMHFYETCP
3989       ----RSASYLKEALLLALADSHHGSSGVT-SPLDVA----LKLAAYKSFSDLSP
```

FIG. 13C

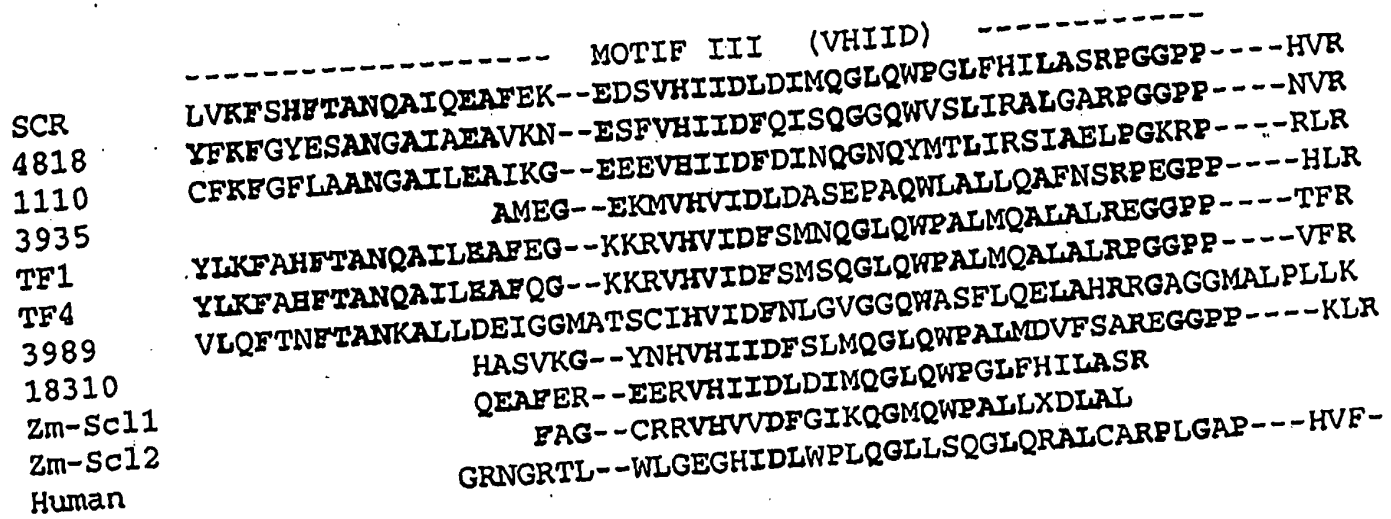

MOTIF III (VHIID)
SCR
4818
1110
3935
TF1
TF4
3989
18310
Zm-Sc11
Zm-Sc12
Human

FIG. 15D

```
                                                                |-------------- MOTIF  V  -
          --||-------------- MOTIF  IV  (DIMERIZATION ) ------------------|
SCR       LTG  LGTSMEA       LQATGKR  LSDFTDK  LGLPFEFCPLAEKVGNDLTERLNV
4818      ITGIDDPRSSFARQGG   LELVGQR  LGKLAEM  CGVPFEFHGAALCCTEVEIEKLGV
1110      LTGIDDPESVQRSIGG   LRIINLR  LEQLAED  NGVSFKFKAMPSKTSIVSPSTLGC
3935      ITG  VHHQKEV       LEQMAHR  LIEEAEK  LDIPFQFNPVVSRLDCLNVEQLRV
TF1       LTGIGPPAPDNSDH     LHEVGCK  LAQLAEA  IHVEFEYRGF  VANSLAD  LDASMLELRP
TF4       LTGIGPPAPDNFDY     LHEVGCK  LAHLAEA  IHVEFEYRGF  VANTLAD  LDASMLELRP
3989      LTAFMSTASHHPLE     LHLTQDN  LSQFAAE  LRIPFEFNAVSLDAFNPAESISSSGDE
18310     ITGIGPNPIGGRDE     LHEVGIR  LAKYAHS  VGIDFTFQGVCVDQLDRLCDWMLLKPI
Human     LPGLHTLS...        LGLQXRH  LLVHMMA  LSYSYGRXP...
```

```
          --------------|
SCR       RKREAAVHWLQHSLYDVTGSDAHTLWLL---QRLAPK------------------
4818      RNGEALAVNFPLVLHHMPDESVTVENHR---DRLLRL------------------
1110      KPGETL VNFAFQLHHMPDESVTTVNQR---DELLHM------------------
3935      KTGEALAVSSVLQLHTFLASDDDLMRKNC-ALRFQNNPSGVDLQRVLMMSHGS
TF1       SDTEAVAVNSVFELHKLLGRXGGIEKVLG------------------------
TF4       SEIESVAVNSVFELHKLLGRPGAIDKVLG------------------------
18310     K-GEAVAINSILQLHRLLVDPDANPVVPAPIDILLK---
3989      VVAVSLPVGCSARAPPLPAILRLVKQLCPKVVVAID
```

FIG. 15E

```
                                                            |----
SCR     ----------------------------------------------VVTV-
4818    ----------------------------------------VKHLSPN-VVTL-
1110    ----------------------------------------VKSLNPK-LVTV-
3935    AAEARENDMSNNNGYSPSGDSASSLPLPSSGRTDSFLNAIWGLSPKVMVVT-
TF1     ----------------------------------------VVKQD*TGDFHXW
TF4     ----------------------------------------VVNQIKPEIFTV-
18310   ----------------------------------------LVIKINPMIFTV-


        -----------------  MOTIF  VI  ---------------------
SCR     VEQDLSHAGS--FLG-RFVEAIHYYSALFDSLGASYGEESE---ERHVVEQQ
4818    VEQEANTNTAP-FLP-RFVETMNHYLAVFESIDVKLARDHK---ERINVEQH
1110    VEQDVNTNTSP-FFP-RFIEAYEYYSAVFESLDMTLPRESQ---ERMNVERQ
3935    -EQDSDHNGS--TLMERLLESLYTYAALFDCLETKVPRTSQ---DRIKVEKM
TF1     XRQEPNHNG-PGFLD-GXTESLHYYSTXFDSLEG--XPNSQ---DKLMSEXY
TF4     VEQESNHNS-PIFLD-RFTESLHYYSTLFDSLEG--VPSGQ---DKVMSEVY
18310   VEHEADHNR-PPLLE-RFTNALFHYATMFDSLEAMHTCTSGRDITDSLTEVY
```

09265585.031099

FIG. 13F

```
          ----------------------------------------
SCR       LLSKEIRNVLAVGGPSRSGEVKFE-SWREKMQQCGFKGIS-
4818      CLAREVVNLIACEGVEREERHEPLGKWRSRFHMAGFKPYP-
1110      CLARDIVNIVACEGEERIERYEAAGKWRARMMMAGFNPKP-
3935      LFGEEIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVP-
TF1       -LGXQICNLVACEGPDRVERHETLSQWGNRFGSSGLAPAH-
TF4       -LGKQICNVVACDGPDRVERHETLSQWRNRFGSAGFAAAH-
18310     -LRGEIFDIVCGEGSARTERHELFGHWRERLTYAGLTQVWF


          ------------------------------------------------|
SCR       LAGNAATQATLLLGMFPS-DGYTLVDDN-GTLKLGWKDLSLLTASAWTPRS*
4818      LSSYVNATIKGLLES-YS-EKYTL-EERDGALYLGWKNQPLITSCAWR*
1110      MSAKVTNNIQNLIKQQYC-NKYKLKEEM-GELHFCWEEKSLIVASAWR*
3935      LSYYAMLQARRLLQGCGF-DGYRIKEES-GCAVICWQDRPLYSVSAWRCRK*
TF1       LGSNAFKQASMLLSVFNSGQGYRV-EESNGCLMLGWHTRPLITTSAWKLSTAAH*
TF4       IGSNAFKQASMLLALFNGGEGYRV-EESDGCLMLGWHTRPLIATSAWKLSTN*
3989         ADCLL-KRVQVRGFHV-EKRGAALTLYWQRGELVSISSWRC*
18310     DPDEVDTLKDQLIHVTSLSGSGFNILVCDGSLALAWHNRPLYVATAWCVTGGNAA


18310     SSMVGNICKGTNDSRRKENRNGPME*
```

FIG. 14

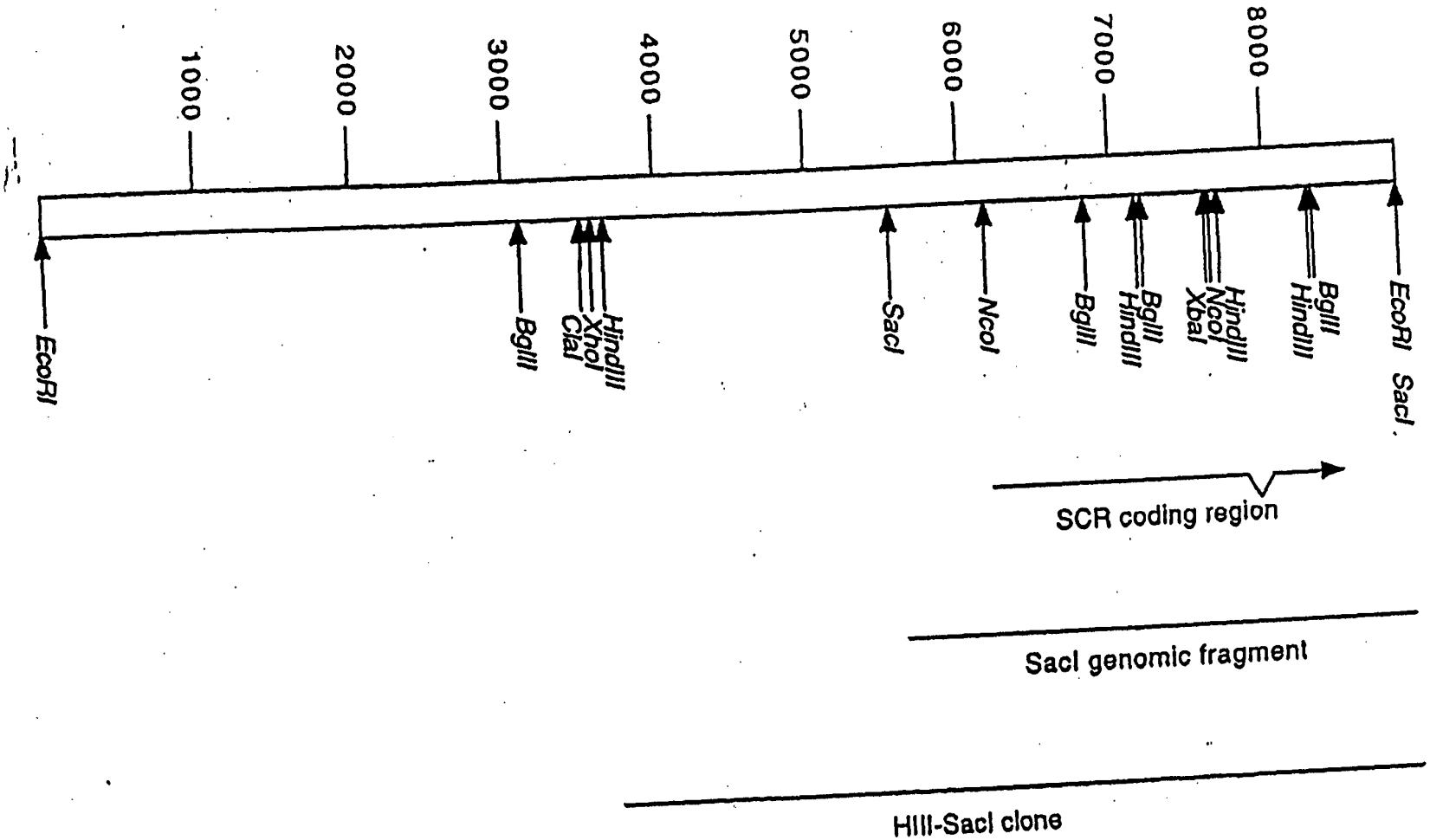


FIG. 15A

Old Name						New Name
Scr	....	....	....	....	....	*SCR*
3989	....	....	....	....	....	*SRPo3*
12398	....	....	....	....	....	*SRPa6*
4871	....	....	....	....	....	*SRPa5*
11846	....	....	....	....	....	*SRPo4*
2504	....	....	....	....	....	*SRPo2*
3935	....	....	....	....	....	*SRPa3*
11261	....	....	....	....	....	*SRPa10*
713	....	....	....	....	....	*SRPo1*
10964	....	....	....	....	....	*SRPa9*
23196	LL	KVLLCHLVAE	STKRRIKIRP	LLDINDSGFL	GFWSWIHMGS	*SRPa12*
Tf1	....	....	....	....	....	*SRPa8*
Tf4	....	....	....	....	....	*SRPa2*
18310	....	....	....	....	....	*SRPm1*
18652	....	....	....	....	....	*SRPa11*
4818	....	....	....	....	....	*SRPa4*
21729	....	....	....	....	....	*SRPa7*
1110	....	....	....	....	....	*SRPa1*
174	....	....	....	....	....	*SRPb1*
33/08	....	....	....	....	....	*SRPa13*
	-150				-101	

FIG. 15B

Scr	....	....	....	....	....
3989	....	....	....	....	....
12398	....	....	....	....	....
4871	....	....	....	....	....
11846	....	....	....	....	....
2504	....	....	....	....	....
3935	....	....	....	....	....
11261	....	....	....	....	....
713	....	....	....	....	....
10964	....	....	....	....	....
23196	YPDGFPGSMD	ELDFNKDFDL	PPSSNQTLGL	ANGFYLDDLD	FSSLDPPEAY
Tf1	....	....	....	....	....
Tf4	....	....	....	....	....
18310	....	....	....	....	....
18652	....	....	....	....	....
4818	....	....	....	....	....
21729	....	....	....	....	....
1110	....	....	....	....	....
174	....	....	....	....	....
33/08	....	....	....	....	....
	-100				-51

FIG. 15C

```
Scr   .......... .......... .......... .......... ..........
3989  .......... .......... .......... .......... ..........
12398 .......... .......... .......... .......... ..........
4871  .......... .......... .......... .......... ..........
11846 .......... .......... .......... .......... ..........
2504  .......... .......... .......... .......... ..........
3935  .......... .......... .......... .......... ..........
11261 .......... .......... .......... .......... ..........
713   .......... .......... .......... .......... ..........
10964 .......... .......... .......... .......... ..........
23196 PSQNNNNNNI NNKAVAGDLL SSSSDDADFS DSVLKYISQV LMEEDMEEKP
Tf1   .......... .......... .......... .......... ..........
Tf4   .......... .......... .......... .......... ..........
18310 .......... .......... .......... .......... ..........
18652 .......... .......... .......... .......... ..........
4818  .......... .......... .......... .......... ..........
21729 .......... .......... .......... .......... ..........
1110  .......... .......... .......... .......... ..........
174   .......... .......... .......... .......... ..........
33/08 .......... .......... .......... .......... ..........
      -50                                                  -1
```

FIG. 15D

```
Scr    MAESGDFNGG QPPPHSPLRT TSSGSSSSNN RGPPPPPPPP LVMVRKRLAS
3989   .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
4871   .......... .......... .......... .......... ..........
11846  .......... .......... .......... .......... ..........
2504   .......... .......... .......... .......... ..........
3935   .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
713    .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  CMFHDALALQ AAEKSLYEAL GEKDPSSSSA SSVDHPERLA SHSPDGSCSG
Tf1    .......... .......... .......... .......... ..........
Tf4    .......... .......... .......... .......... ..........
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
4818   .......... .......... .......... .......... ..........
21729  .......... .......... .......... .......... ..........
1110   .......... .......... .......... .......... ..........
174    .......... .......... .......... .......... ..........
33/08  .......... .......... .....TSDSA SSFNIPTSAQ NHYATGSFST
       1                                                 50
```

FIG. 15E

```
                   |<--------Motif I ---------------------------->|
Scr     EMSSNPDYNN SSRPPRRVSH LLDSNYNTVT PQQPPSLTAA ATVSSQPNPP
3989    .......... .......... .......... .......... ..........
12398   .......... .......... .......... .......... ..........
4871    .......... .......... .......... .......... ..........
11846   .......... .......... .......... .......... ..........
2504    .......... .......... .......... .......... ..........
3935    .......... .......... .......... .......... ..........
11261   .......... .......... .......... .......... ..........
713     .......... .......... .......... .......... ..........
10964   .......... .......... .......... .......... ..........
23196   GAFSDYASTT TTTSSDSHWS VDGLENRPSW LHTPMPSNFV FQSTSRSNSV
Tf1     .......... .MKRDHHQFQ GRLSNHGTSS SSSSISKDKM MMVKKEEDGG
Tf4     .......... .MKRDHHHHH .......... ......QDKK TMMMNEEDDG
18310   .......... .......... .......... .......... ..........
18652   .......... .......... .......... .......... ..........
4818    .......... .......... .......... .......... ..........
21729   .......... .......... .......... .......... ..........
1110    .......... .......... .......... .......... ..........
174     .......... .......... .......... .......... ..........
33/08   NSRTTNVATA TTNSATAHWV ATDAEHTDTI IAQP
        51                                              100
```

FIG. 15F

Scr	LSVCGFSGLP	VFPSDRGGRN	VMMSVQPMDQ	DSSSSSASPT	VWVDAIIRDL
3989	....	....	....	....	....
12398	....	....	....	....	....
4871	....	....	....	....	....
11846	....	....	....	....	....
2504	....	....	....	....	....
3935	....	....	....	....	....
11261	....	....	....	....	....
713	....	....	....	....	....
10964	....	....	....	....	....
23196	TGGGGGGNSA	VYGSGFGDDL	VSNMFKDDEL	AMQFKKGVEE	ASKFLPKSSQ
Tf1	GNMDDELLAV	LGYKVRSSEM	AEVALKLEQL	ETMMSNAQED	GLSHLATDAA
Tf4	NGM.DELLAV	LGYKVRSSEM	ADVAQKLEQL	EVMMSNVQED	DLSQLATETV
18310	....	....	....	....	....
18652	....	....	....	....	....
4818	....	....	....	....	....
21729	....	....	....	....	.........D
1110	....	....	....	....	....
174	....	....	....	....	....
	101				150

FIG. 15G

Scr	IHSSTSVSIP	QLIQNVRDII	FPCNPNLGAL	LEYRLRSLML	LDPSSSSDPS
3989	....	....	....	....	....
12398	....	....	....	....	....
4871	....	....	....	....	....
11846	....	....	....	....	....
2504	....	....	....	....	....
3935	....	....	....	....	....
11261	....	....	....	....	....
713	....	....	....	....	....
10964	....	....	....	....	....
23196	LFIDVDSYIP	MNSGSKENGS	EVFVKTEKKD	ETEHHHHHSY	APPPNRLTGK
Tf1	HYNPSELYSW	LDNMLSELNP	PPLPASSNGL	DPVLPSPEIC	GFPXSDYDLK
Tf4	HYNPAELYTW	LDSMLTDLNP	P....SSNA.	....	.....EYDLK
18310	....	....	....	....	....
18652	....	....	....	....	....
4818	....	....	....	....	....
21729	LTSVNDMSLF	GGSGSSQRYG	LPVPRSQTQQ	QQSDYGLFGG	IRMGIGSGIN
1110	....	....	....	....	....
174	....	....	....	....	....
	151				200

FIG. 15H

```
  Scr  PQTFEPLYQI SNNPSPPQQQ QQHQQQQQQH KPPPPPIQQQ ERENSSTDAP
 3989  .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
 4871  .......... .......... .......... .......... ..........
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  KSHWRDEDED VEERSNKQSA VYVEESELSE MFDNMFLCGP GKPVCILNQN
  Tf1  VIPXNAIYQF PAIDSSSSSN NQ........ NKRLKSCSSP DSMVTSTSTG
  Tf4  AIPGDAILNQ FAIDSASSSN QGGGGDTYTT NKRLKCS... ..........
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
 4818  .......... .......... .......... .......... ..........
21729  NYPTLTGVPC IEPVQNRVHE SENMLNSLRE LEKQLLDDDD ESGGDDDVSV
 1110  .......... .......... .......... .......... ..........
  174  .......... .......... .......... .......... ..........
       201                                             250
```

FIG. 15I

```
                    |<--- bZIP like domain --->|
                          |<-- Motif II (dimerization) ----------
  Scr  PQPETVTATV PAVQTNTAEA LRERKEEIKR QKQDEEGLHL LTLLLQCAEA
 3989  .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
 4871  .......... .......... ....AAIFYG HHHHTPPPAK RLNPGPVGIT
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  NFPTESAKVV TAQSNGAKIR GKKSTSTSHS NDSKKETADL RTLLVLCAQA
  Tf1  TQIGGVIGTT VTTTTTTTTA AAESTRSVIL VDSQENGVRL VHALMACAEA
  Tf4  ...NGVVE.. ......TTTA TAESTRHVVL VDSQENGVRL VHALLACAEA
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
 4818  .......... .......... .......... .......... ..........
21729  ITNSNSDWIQ NLVTPNPNPN PVLSFSPSSS SSSSSPSTAS TTTSVCSRQT
 1110  .......... .......... .......... .......... ..........
  174  .......... .......... .......... .......... ..........
       251                                                  300
```

FIG. 15J

```
       ------ Motif II (dimerization) ------------→|
Scr    VSADNLEEAN KLLLEISQLS TPYGTSAQRV AAYFSEAMSA RLLNSCLGIY
3989   .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
4871   EQLVKAAEVI ESDTCLAQGIL ARLNQQLSS PVGKPLERAA FYFKEALNNL
11846  .......... .......... .......... .......... ..........
2504   .......... .......... .......... .......... ..........
3935   .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
713    .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  VSVDDRRTAN EMLRQIREHS SPLGNGSERL AHYFANSLEA RLAGTGTQIY
Tf1    IQQNNLTLAE ALVKQIGCLA VSQAGAMRKV ATYFAEALAR RIYRLSPPQN
Tf4    VQKENLTVAE ALVKQIGFLA VSQIGAMRQV ATYFAEALAR RIYRLSPSQS
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
4818   .......... .......... .......... .......... ........GT
21729  VMEIATAIAE GKTEIATEIL ARVSQTPNLE RNSEEKLVDF MVAALRSRIA
1110   ...LSMVNEL RQIVSIQGDP SQRIAAYMVE GLAARMAASG KFIYRALKCK
174    .......... .......... .......... .......... ..........
       301                                               350
```

FIG. 15K

```
                                        |<-- Motif III (SCR VHIID) ---
  Scr   AALPSRWMPQ THSLKMVSAF QVFNGISPLV KFSHFTANQA IQEAFEKEDS
 3989   .......... .......... .......... ..LYRNKALL DEIGGMATSC
12398   .......... .......... .......... .......... ..........
 4871   LHNVSQTLSA CSLIFKVAAY KSFSEISPVL QFANFTSNQA LLESFHGFHR
11846   .......... .......... .......... .......... ..........
 2504   .......... .......... .......... .......... ..........
 3935   .......... .......... .......... .......... ...AMEGEKM
11261   .......... .......... .......... .......... ..........
  713   .......... .......... .......... .......... ..........
10964   .......... .......... .......... .......... ..........
23196   TALS...SKK TSAADMLKAY QTYMSVCPFK KAAIIFANHS MMRFTANANT
  Tf1   QIDHCLSDT. ........LQ MHFYETCPYL KFAHFTANQA ILEAFEGKKR
  Tf4   PIDHSLSDT. ........LQ MHFYETCPYL KFAHFTANQA ILEAFQGKKR
18310   .......... .......... .......... ........HA SVKGYN...H
18652   .......... .......... .......... ......ANVE ILEAIAGETR
 4818   SPTGPELLT. ........YM HILYEACPYF KFGYESANGA IAEAVKNESF
21729   SPVTELYGKE HLISTQL... ..LYELSPCF KLGFEAANLA ILDAADNNDGGMMI
 1110   EPPSDERLA. ........AM QVLFEVCPCF KFGFLAANGA ILEAIKGEEE
  174   .......... .......... .......... .......... ..........
        351                                                   400
```

FIG. 15L

```
        -- Motif III (VHIID) ---------------->|<- -- Motif IV ---
  Scr   VHIIDLDIMQ GLQWPGLFHI LASRPGGPPH VRLTGLGTSM EA......LQ
 3989   IHVIDFDLGV GGQWASFLQE LAHRRGAGGM ALPLLKLTAF MSTASHHPLE LH
12398   .......... .......... .......... .......... ..........
 4871   LHIIDFDIGY GGQWASLMQE LVLRDNAAPLSLKITVFASPA NHVQLELG..
11846   .......... .......... .......... .......... ..........
 2504   .......... .......... .......... .......... ..........
 3935   VHVIDLDASE PAQWLALLQA FNSRPEGPPH LRITGVHHQK EVLE......
11261   .......... .......... .......... .......... ..........
  713   .......... .......... .......... .......... ..........
10964   .......... .......... .......... .......... ..........
23196   IHIIDFGISY GFQWPALIHRLSLSRPGGSPK LRITGIELPQ RGFRPAE...
  Tf1   VHVIDFSMNQ GLQWPALMQA LALREGGPPT FRLTGIGPPA PDNSDHLH..
  Tf4   VHVIDFSMSQ GLQWPALMQA LALRPGGPPV FRLTGIGPPA PDNFDYLH..
18310   VHIIDFSLMQ GLQWPALMDV FSAREGGPPK LRITGIGPNP IGGRDELH..
18652   VHIIDFQIAQ GSQYMFLIQE LAKRPGG... ...PPLLRVT GVDDSQSTYARGGGLS
 4818   VHIIDFQISQ GGQWVSLIRA LGARPGG... ...PPNVRIT GIDDPRSSFARQGGLE
 1110   VHIIDFDINQ GNQYMTLIRS IAELPGK... ...RPRLRLT GIDDPESVQRSIGGLR
21729   PHVIDFDIGE GGQYVNLLRT LSTRRNGKSQ SQNSPVVKIT AVANNVYGDCLVDDGGEERLK
  174   .......... .......... .......... .......... ..........
        401                                                   450
```

FIG. 15M

```
                     |← --- Motif V ----------------------------
       --- Motif IV-------------------------------→|
  Scr  ATGKRLSDFT DKLGLPFEFC PLAEKVGNDL TERLNVRKRE AVAVHWL...
 3989  LHLTQDNLSQ FAAELRIPFE FNAVSLDAFN PAESISSSGD EVVAVSL...
12398  .......... .......... .......... .......... ..........
 4871  FTQDNLKHFA SEINISLDIQ VL..SLDLLG SISWPNSS.. EKEAVAVNIS
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .....NGGAF APSTWTA...
 3935  QMAHRLIEEA EKLDIPFQFN PVVSRLDCLN VE...QLRVK TGEALAVSSV
11261  .......... .......... .........K KWETITLDEL MINPGETTVV
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  EFRRQVIAWL DTVSDTMFRL STTQLLRNGE TIQVEDLKLR QGEYVVVNSL
  Tf1  EVGCKLAQLA EAIHVEFEYR GFVANSLADL DASMLELRPS DTEAVAVNSV
  Tf4  EVGCKLAHLA EAIHVEFEYR GFVANTLADL DASMLELRPS EIESVAVNSV
18310  EVGIRLAKYA HSVGIDFTFQ GVCVDQLDRL CDWML.LKPI KGEAVAINSI
18652  LVGERLATLA QSCGVPFEFH D...AIMSGC KVQREHLGLE PGFAVVVNFP
 4818  LVGQRLGKLA EMCGVPFEFH G...AALFCT EVEIEKLGVR NGEALAVNFP
21729  AVGDLLSQLG DHSISVSFNV V...TSLRLG DLNRESLGCD PDETLAVNLA
 1110  IIGLRLEQLA EDNGVSFKFK A...MPSKTS IVSPSTLGCK PGETLIVNFA
  174  .......... .......... .......... .......... ..........
       451                                              500
```

FIG. 15N

```
        ----- Motif V ----------------------------------------
  Scr   ...QHS.... .......... .......... .......... ..........
 3989   .........P VG........ .......... .......... ..........
12398   .......... .......... .......... .......... ..........
 4871   .....AA... .......... .......... .......... ..........
11846   .......... .......... .......... .......... ..........
 2504   .........R SL........ .......... .......... ..........
 3935   LQLHTFLASD DDLMRKNCAL RFHNNPSGVD LQRVLMMSHG SAAEARENDM
11261   NCIHRLQYTP DE........ .......... .......... ..........
  713   .......... .......... .......... .......... ..........
10964   .......... .......... .......... .......... ..........
23196   FRFRNLL... DE........ .......... .......... ..........
  Tf1   FELHKLLGRX GG........ .......... .......... ..........
  Tf4   FELHKLLGRP GA........ .......... .......... ..........
18310   LQLHRLLVDP DA........ .......... .......... ..........
18652   YVLHHM...P DE........ .......... .......... ..........
 4818   LVLHHM...P DE........ .......... .......... ..........
21729   FKLYRV...P DE........ .......... .......... ..........
 1110   FQLHHM...P DE........ .......... .......... ..........
  174   .......... .......... .......... .......... ..........
        501                                                 550
```

FIG. 150

```
          Motif V ---------→|                         |←-- Motif VI ---
  Scr     .......... ......LYDVTGSD AHTLWLLQRL APKVVTVVEQ DLSHAGS.FL
 3989     .......... ......CSARAPPL PAILRLVKQL CPKVVVAIDH GGDRADLPFS
12398     .......... .............. .......... .......... ..........
 4871     .......... ......SFSHLPLV LRFVKHLSPT IIVCSDRGCE RTDLPFSQQL
11846     .......... .............. .......... .........Q EADHNKTGFL
 2504     .NGGAFAPST WTARSLPVPSSPST DSF....... .......... ..........
 3935     SNNNGYSPSG DSASSLPLPSSGRT DSFLNAIWGL SPKVMVVTEQ DSDHNGSTLM
11261     .......... ......TVSLDSPR DTVLKLFRDI NPDLFVFAEI NGMYNSPFFM
  713     .......... .............. .......... .......... NGSYNAPFFV
10964     .......... .............. .......... .......... ..AYNAPFFV
23196     .......... ......TVLVNSPR DAVLKLIRKI NPNVFIPAIL SGNYNAPFFV
  Tf1     .......... .............I EKVLGVVKQD TGDFHXWXRQ EPNHNGPGFL
  Tf4     .......... .............I DKVLGVVNQI KPEIFTVVEQ ESNHNSPIFL
18310     .......... ......NPVVPAPI DILLKLVIKI NPMIFTVVEH EADHNRPPLL
18652     .......... ......SVSVEKYR DRLLHLIKSL SPNLVTLVEQ EDNTNTSPLV
 4818     .......... ......SVTVENHR DRLLRLVKHL SPNVVTLVEQ EANTNTAPFL
21729     .......... ......SVCTENPR DELLRRVKGL KPRVVTLVEQ EMNSNTAPFL
 1110     .......... ......SVTTVNQR DELLHMVKSL NPKLVTVVEQ DVNTNTSPFF
  174     .......... .............. .......... .......... ..........
          551                                                    600
```

FIG. 15P

```
       ------- Motif VI ------------------------------------
  Scr  GRFVEAIHYY SALFDSLGAS Y..GEESEER HVVEQQLLSK EIRNVLAVGG
 3989  QHFLNCFQSC VFLDSLDAAG I..DADSA.. CKIERFLIQP RVEDAVIG..
12398  .......... .....SLEPN L..DRDSKER LRVERVLFGR RIMDLVRSDD
 4871  AHSLHSHTAL FESLDAVNAN L..DAM.... QKIERFLIQP EIEKLVLD..
11846  DRFTEALFYY SAVFDSLDAA N..NNNNNNN QRMEAEYLQR EICDIVCGEG
 2504  .......... .......... .......... .......... ..........
 3935  ERLLESLYTY AALFDCLETK V..PRTSQDR IKVEKMLFGE EIKNIISCEG
11261  TRFREALFHY SSLFDMFDTT IHAEDEYKNR SLLERELLVR DAMRVISCEG
  713  TRFREALFHY SAIFDMLETN I..PKDNEQR LLIESALFSR E.XNVISCEG
10964  TRFREALFHF SSIFDMLETI V..PREDEER MFLEMEVFGR EALNVIACEG
23196  TRFREALFHY SAVFDMCDSK L..AREDEMR LMYVFEFYGR EIVNVVASEG
  Tf1  DGXTESLHYY STXFDSLEGX ...PNSQD.. KLMSEXYLGX QICNLVACEG
  Tf4  DRFTESLHYY STLFDSLEGV ...PSGQD.. KVMSEVYLGK QICNVVACDG
18310  ERFTNALFHY ATMFDSLEAM HRCTSGRDIT DSLTEVYLRG EIFDIVCGEG
18652  SRFVETLDYY TAMFESIDAA R..PRDDKQR ISAEQHCVAR DIVNMIACEE
 4818  PRFVETMNHY LAVFESIDVK L..ARDHKER INVEQHCLAR EVENLIACEG
21729  GRVSESCACY GALLESVEST V..PSTNSDR AKVE.EGIGR KLVNAVACEG
 1110  PRFIEAYEYY SAVFESLDMT L..PRESQER MNVERQCLAR DIVNIVACEG
  174  .......... .RXFDSLEHD A..SKGEPRE DERGRXCLAR NIVNIVXCKX
       601                                                650
```

FIG. 15Q

```
Scr    PSRSGEVKF. .....ESWRE KMQQCGFKGI SLAG..NAAT QATLLLGMFP
3989   .RHKA..Q.. ...KAIAWRS VFAATGFKPV QLSN..LAEA QADCLLKRVQ
12398  DNNKPGTRFG LMEEKEQWRV LMEKAGFEPV KPSN..YAVS QAKLLLWNYN
4871   .RSRPIER.. ...PMMTWQA MFLQMGFSPV THSN..FTES QAECLVQRTP
11846  AARXERHE.. ...PLSRWRD RLTRAGLSAV PLG....SNA ..........
2504   .......... .......... .......... PLSY..YAML QARRLLQGCG
3935   FERRERHE.. ...KLEKWSQ RIDLAGFGNV PLSY..YAML QARRLLQGCG
```

```
Scr    PSRSGEVKF. .....ESWRE KMQQCGFKGI SLAG..NAAT QATLLLGMFP
3989   .RHKA..Q.. ...KAIAWRS VFAATGFKPV QLSN..LAEA QADCLLKRVQ
12398  DNNKPGTRFG LMEEKEQWRV LMEKAGFEPV KPSN..YAVS QAKLLLWNYN
4871   .RSRPIER.. ...PMMTWQA MFLQMGFSPV THSN..FTES QAECLVQRTP
11846  AARXERHE.. ...PLSRWRD RLTRAGLSAV PLG....SNA ..........
2504   .......... .......... .......... .......... ..........
3935   FERRERHE.. ...KLEKWSQ RIDLAGFGNV PLSY..YAML QARRLLQGCG
11261  AERFARPE.. ...TYKQWRV RILRAGFKPA TIS....KQI MKEAKEIVRK
713    LERMERPE.. ...TYKQWQV RNQRVGFKQL PLN....QDM MKRARXEGQV
10964  WERVERPE.. ...TYKQWHV RAMRSGLVQV PFD....PSI MKTSLHKVHT
23196  TERVESRE.. ...TYKQWQA RLIRAGFRQL PLE....KEL MQNLKLKIEN
Tf1    PDRVERHE.. ...TLSQWGN RFGSSGLAPA HLGS...NAF KQASMLLSVF
Tf4    PDRVERHE.. ...TLSQWRN RFGSAGFAAA HIGS...NAF KQASMLLALF
18310  SARTERHE.. ...LFGHWRE RLTYAGLTQV WFDPDEVDTL KDQLIHVTSL
18652  SERVERHE.. ...VLGKWRV RMMMAGFTGW PVSTSAAFAA SE....MLK.
4818   VEREERHE.. ...PLGKWRS RFHMAGFKPY PLSSYVNATI KG....LLE.
21729  IDRIERCE.. ...VFGKWRM RMSMAGFELM PLSEKIAESM KS....RGNR
1110   EERIERYE.. ...AAGKWRA RMMMAGFNPK PMSAKVTNNI QN....LIKQ
174    EERIERYE.. ...VTGKWRA RMMMAGFSPR PMSGRVTSNI ES....LIKR
       651                                                700
```

FIG. 15R

```
       ----- Motif VI ------------------→|
  Scr  .SDGYTLVD. DNGTLKLGWK DLSLLTASAW TPRSX..... ..........
 3989  VRGFH..VEK RGAALTLYWQ RGELVSISSW RCX....... ..........
12398  YSTLYSLVES EPGFISLAWN NVPLLTVSSW RX........ ..........
 4871  VRGFH..VEE KHNSLLLCWQ RTELVGVSAW RCRSSX.... ..........
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  FDGYR..IKE ESGCAVICWQ DRPLYSVSAW RCRKX..... ..........
11261  RYHRDFVIDS DNNWMLQGWK GRVIYAFSCW KPAEKFTNNN LNIX......
  713  LPTRTFIIDE DNRWLLQGWK GRILFALSTW KPDNRSSSX. ..........
10964  FYHKDFVIDQ DNRWLLQGWK GRTVMALSVW KPESX..... ..........
23196  GYDKNFDVDQ NGNWLLQGWK GRIVYASSLW VPSSSX.... ..........
  Tf1  NSGQGYRVEE SNGCLMLGWH TRPLITTSAW KLSTAAHX.. ..........
  Tf4  NGGEGYRVEE SDGCLMLGWH TRPLIATSAW KLSTNX.... ..........
18310  .SGSGFNILV CDGSLALAWH NRPLYVATAW CVTGGNAASS MVGNICKGTN
18652  AYDKNYKLGG HEGALYLFWK RRPMATCSVW KPNPNYIGX. ..........
 4818  SYSEKYTLEE RDGALYLGWK NQPLITSCAW RX........ ..........
21729  VHPG.FTVKE DNGGVCFGWM GRALTVASAW RX........ ..........
 1110  QYCNKYKLKE EMGELHFCWE EKSLIVASAW RX........ ..........
  174  DYCSKYKVKE EMGELHFSWE EKSLIVASAW SX........ ..........
       701                                             750
```

FIG. 15S

```
Scr     .......... ....
3989    .......... ....
12398   .......... ....
4871    .......... ....
11846   .......... ....
2504    .......... ....
3935    .......... ....
11261   .......... ....
713     .......... ....
10964   .......... ....
23196   .......... ....
Tf1     .......... ....
Tf4     .......... ....
18310   DSRRKENRNG PMEX
18652   .......... ....
4818    .......... ....
21729   .......... ....
1110    .......... ....
174     .......... ....
          751        764
```

FIG. 16A

SRPa1 (1110)

CTTTGTCAATGGTAAATGAGCTGAGGCAGATAGTTTCTATCCAAGGAGACCCTTCTCAGA
GAATCGCAGCTTACATGGTGGAAGGTCTAGCTGCAAGAATGGCCGCTTCAGGAAAATTCA
TCTACAGAGCATTGAAATGCAAAGAGCCTCCTTCGGATGAGAGGCTTGCAGCTATGCAAG
TCCTGTTTGAAGTCTGCCCTTGTTTCAAGTTCGGGTTTTTAGCAGCTAATGGTGCGATAC
TTGAAGCAATCAAAGGTGAAGAAGAAGTTCACATAATCGATTTCGATATAAACCAAGGGA
ACCAATACATGACACTGATACGAAGCATTGCTGAGTTGCCTGGTAAACGACCTCGCCTGA
GGTTAACAGGAATTGATGACCCTGAATCAGTCCAACGCTCCATTGGAGGGCTAAGAATCA
TCGGTCTAAGACTCGAGCAACTCGCAGAGGATAATGGAGTATCCTTCAAATTCAAAGCAA
TGCCTTCAAAGACTTCGATTGTCTCTCCATCAACACTCGGTTGCAAACCAGGAGAAACCT
TAATAGTGAACTTTGCATTCCAACTTCACCACATGCCTGACGAGAGTGTCACAACAGTAA
ACCAGCGGGACGAGCTACTTCACATGGTCAAAAGCTTAAACCCAAAGCTTGTCACGGTCG
TTGAACAAGACGTGAACACAAACACTTCACCGTTCTTTCCCAGATTCATAGAGGCTTACG
AATACTACTCAGCAGTTTTCGAGTCTCTAGACATGACACTTCCAAGAGAAAGCCAAGAGA
GGATGAATGTAGAAAGACAGTGTCTCGCTAGAGACATAGTCAACATTGTTGCTTGCGAAG
GAGAAGAACGGATAGAGAGATACGAGGCTGCGGGAAAATGGAGAGCAAGGATGATGATGG
CTGGATTCAATCCAAAACCAATGAGTGCTAAAGTAACCAACAATATACAAAACCTGATAA
AGCAACAATATTGCAATAAGTACAAGCTTAAAGAAGAAATGGGTGAGCTCCATTTTTGCT
GGGAGGAGAAAAGCTTAATCGTTGCTTCAGCTTGGAGGTAAGATAAGTGACAAGAGCATA
TAGTCTTTATGTTTCATAAAACATAATTATGTTTTTACTGTAATCTTGGGTTATTGTGTA
ACTGGTTAAATCATCTCCATGTATTATTACCAGAGGTTAGGGGTGATCACAGGTACTAAA
AGCTAATCTAACACTTATGGAAGAATTTTTCTTTCTTTTTTTTCCCTATTATATAAAAAT
AATTAGAGTTTTGGTTCTAAACCTATTTGCTAAGTGTGAATGAGTCTTTACATGTTCATA
TTTCAGTTCAAATGGTTAAATTTGTTAAGGTTCTCACTTAAAAAAAAA

FIG. 16B

SRPa3 (3935)

GCTATGGAAGGAGAGAAGATGGTTCATGTGATTGATCTCGATGCTTCTGAGCCAGCTCAA
TGGCTTGCTTTGCTTCAAGCTTTTAACTCTAGGCCTGAAGGTCCACCTCATTTGAGAATC
ACTGGTGTTCATCACCAGAAGGAAGTGCTTGAACAAATGGCTCATAGACTCATTGAGGAA
GCAGAGAAACTCGATATCCCGTTTCAGTTTAATCCCGTTGTGAGTAGGTTAGACTGTTTA
AATGTAGAACAGTTGCGGGTTAAAACAGGAGAGGCCTTAGCCGTTAGCTCGGTTCTTCAA
TTGCATACCTTCTTGGCCTCTGATGATGATCTCATGAGAAAGAACTGCGCTTTACGGTTT
CAGAACAACCCTAGTGGAGTTGACTTGCAGAGAGTTCTAATGATGAGCCATGGCTCTGCA
GCTGAGGCACGTGAGAATGATATGAGTAACAACAATGGGTATAGCCCTAGCGGTGACTCG
GCCTCATCTTTGCCTTTACCAAGTTCAGGAAGGACTGATAGCTTCCTCAATGCTATTTGG
GGTTTGTCTCCAAAGGTCATGGTGGTCACTGAGCAAGACTCAGACCACAACGGCTCCACA
CTAATGGAGAGGCTATTAGAATCACTTTACACCTACGCAGCATTGTTTGATTGCTTGGAA
ACAAAAGTTCCAAGAACGTCTCAAGATAGGATCAAAGTGGAGAAGATGCTCTTCGGGGAG
GAGATCAAGAACATCATATCCTGCGAGGGATTTGAGAGAAGAGAAAGACACGAGAAGCTT
GAGAAATGGAGCCAGAGGATCGATTTGGCTGGTTTTGGGAATGTTCCTCTTAGCTATTAT
GCGATGTTGCAGGCTAGGAGATTGCTTCAAGGGTGCGGTTTTGATGGGTATAGAATCAAG
GAAGAGAGCGGGTGCGCAGTAATTTGCTGGCAAGATCGACCTCTATACTCGGTATCAGCT
TGGAGATGCAGGAAGTGAATGATATATTACAGTTTGTCTTCTATTTTGGTTATGAGCAGA
GTCCCTTTCTTTTTTGTATACATGGGGACACAATCTTAGTTGTTTTGTGATGGTGACTTT
CTGTCTCTTTATGCTATTTTGGCTTAAATGCTTCTACTGCCTCTGCATGTAAAGCCTTTG
TGTGTTGGTTCAATTTGGTCTGGTGTGGGTGTAATACCAAACCAAATCCAATTTGAGCTG
AAGATAACTAATTTGATGATCGGCTCGTGCC

FIG. 16C

SRPa4 (4818)

GGCACGAGCCCAACGGGTCCTGAGCTTCTTACTTATATGCATATCTTGTATGAAGCCTGC
CCTTATTTCAAATTCGGTTATGAATCTGCTAATGGAGCTATAGCTGAAGCTGTGAAGAAC
GAAAGTTTTGTGCACATTATCGATTTCCAGATTTCTCAAGGTGGTCAATGGGTGAGTTTG
ATCCGTGCTCTTGGTGCTAGACCTGGTGGACCTCCGAACGTTAGGATAACGGGAATTGAT
GATCCGAGATCATCGTTTGCTCGTCAAGGAGGACTTGAGTTAGTTGGACAAAGACTTGGG
AAGCTAGCTGAAATGTGCGGTGTTCCGTTTGAGTTCCATGGAGCTGCTTTATGCTGCACG
GAAGTCGAAATCGAGAAGCTAGGAGTTAGAAATGGAGAAGCGCTCGCGGTTAACTTCCCG
CTTGTTCTTCACCACATGCCTGATGAGAGTGTAACTGTGGAGAATCACAGAGATAGATTG
TTGAGATTGGTCAAACACTTGTCACCAAACGTTGTGACTCTGGTTGAGCAAGAAGCGAAT
ACAAACACTGCGCCGTTTCTTCCCCGGTTTGTCGAGACAATGAACCATTACTTGGCAGTT
TTCGAATCAATAGATGTGAAACTCGCTAGAGATCACAAGGAAAGGATCAATGTTGAGCAG
CATTGTTTGGCTAGAGAGGTTGTGAATCTTATAGCTTGTGAAGGTGTTGAAAGAGAAGAG
AGGCACGAGCCACTAGGGAAATGGAGGTCTCGGTTTCACATGGCGGGATTTAAACCGTAT
CCTTTGAGCTCGTATGTGAACGCAACAATCAAAGGATTGCTTGAGAGTTATTCAGAGAAG
TATACACTTGAAGAAAGAGATGGAGCATTGTATTTAGGATGGAAGAATCAACCTCTTATC
ACTTCTTGTGCTTGGAGGTAACTAATAAAAACCTTGTTCGGTTTCAGAAGAGATTAGAAA
CTTCTTTTAAAGTTTGCAGAATCTGTTTGTAAAAGTAAAACTCATGCATGATCCGNAGGA
ACAAGTTGTCAAATGTTGTAGTAGTAAGTGATATGTTGATGACCCAAAAAAAAAAAAAAA
AAAAA

FIG. 16D

SRPa5 (4871)

GCGGCTATCTTCTACGGCCACCACCACCATACACCTCCGCCGGCAAAGCGGCTCAACCCT
GGTCCCGTGGGGATAACAGAGCAGCTGGTTAAGGCAGCAGAGGTCATAGAGAGCGACACG
TGTCTAGCTCAGGGGATATTGGCGCGGCTCAATCAACAGCTCTCTTCTCCCGTCGGGAAG
CCATTAGAAAGAGCAGCTTTTTACTTCAAAGAAGCTCTCAATAATCTCCTTCACAACGTC
TCCCAAACCCTAAACCCTTATTCCCTCATCTTCAAGATCGCTGCTTACAAATCCTTCTCA
GAGATCTCTCCCGTTCTTCAGTTCGCCAACTTTACCTCCAACCAAGCCCTCTTAGAGTCC
TTCCATGGCTTCCACCGTCTCCACATCATCGACTTCGATATCGGCTACGGTGGCCAATGG
GCTTCCCTCATGCAAGAGCTTGTTCTCCGCGACAACGCCGCTCCTCTCTCCCTCAAGATC
ACCGTTTTCGCTTCTCCGGCGAACCACGACCAGCTCGAACTTGGCTTCACTCAAGACAAC
CTCAAGCACTTCGCCTCTGAGATCAACATCTCCCTTGACATCCAAGTTTTGAGCTTAGAC
CTCCTCGGCTCCATCTCGTGGCCTAACTCGTCGGAGAAAGAAGCTGTCGCCGTTAACATC
TCCGCCGCGTCCTTCTCGCACCTCCCTTTGGTCCTCCGTTTCGTGAAGCATCTATCTCCG
ACGATCATCGTCTGCTCCGACAGAGGATGCGAGAGGACGGATCTGCCCTTCTCTCAACAG
CTCGCCCACTCGCTGCACTCACACACCGCTCTCTTCGAATCCCTCGACGCCGTCAACGCC
AACCTCGACGCAATGCAGAAGATCGAGAGGTTTCTTATACAGCCGGAGATAGAGAAGCTG
GTGTTGGATCGTAGCCGTCCGATAGAAAGGCCGATGATGACGTGGCAAGCGATGTTTCTA
CAGATGGGTTTCTCACCGGTGACGCACAGTAACTTCACGGAGTCTCAAGCCGAGTGTTTA
GTCCAACGGACGCCAGTGAGAGGCTTTCACGTCGAGAAGAAACATAACTCACTTCTCCTA
TGTTGGCAAAGGACAGAACTCGTCGGAGTTTCAGCATGGAGATGTCGCTCCTCCTGATTT
CCACCGGAGTTTCAATTATTAAAAAAATATTTTCCTTAATTCAATTTATCTTAAATGACA
AATTTTTAGTTTCTGATTTTATTTTGCTCAGTGCGATGGATTTTTAAATTTAAGTTTCAC
ACAAATATATAAATTTTTG

FIG. 16E

SRPa6 (12398)

AATCGCTTGAACCGAATTTGGATCGAGATTCGAAAGAAAGGCTGAGAGTGGAGAGAGTGC
TGTTCGGTAGGAGGATTATGGATTTGGTCCGATCAGATGATGATAATAATAAACCGGGAA
CCCGGTTTGGGTTAATGGAGGAGAAAGAACAATGGAGAGTGTTGATGGAGAAAGCTGGAT
TTGAGCCGGTTAAACCGAGTAATTACGCGGTTAGCCAAGCGAAGCTGCTACTATGGAACT
ACAATTATAGTACATTGTATTCACTTGTTGAATCGGAGCCAGGTTTCATCTCCTTGGCTT
GGAACAATGTGCCTCTCCTCACCGTTTCCTCTTGGCGTTGACTACTTGGTCCGATAAGTT
AATCTAGTATTTTGAGTTAGCTTTTAGAATTGAATTGTTTGGGGTTAGATTTGGATGTTT
AATTAGTCTCTAGCCTATTCTCTTACTCTTTTTTGTCTAGTGCTTGGAGTGATGATGGTT
TGTCGTTTATGTTCATTTGTAATATATATTGTATGTAACATTTGACTAAAAAAAAAAAAA
AAAAAAAA

FIG. 16F

<u>**SRPa7 (21729/3635/17410)**</u>

AAAGACTTTAGCAGATTTTCAAGCGGCTCAGAACATCAACAACAACAACAACAACAACCG
TTTTATAGTCAAGCAGCTCTCAACGCTTTTCTTTCAAGGTCTGTGAAGCCTCGAAATTAT
CAGAATTTTCAATCTCCGTCGGCCGATGATTGATCTCACGTCGGTGAATGATATGAGTTT
GTTTGGTGGTTCTGGTTCATCTCAGCGTTACGGTTTACCGGTTCCCAGGTCTCAGACGCA
ACAGCAACAATCGGATTACGGTTTATTTGGTGGGATCCGAATGGGAATCGGGTCGGGTAT
TAATAATTATCCAACATTAACCGGCGTTCCGTGTATTGAACCGGTTCAAAACCGGGTTCA
TGAATCGGAGAACATGTTGAATAGTTTAAGAGAGCTTGAGAAACAGCTTTTAGATGATGA
CGATGAGAGTGGTGGTGATGATGACGTGTCAGTTATAACAAATTCAAATTCCGATTGGAT
TCAAAATCTCGTGACTCCGAACCCGAACCCGAACCCGGTTTTGTCTTTTTCACCGAGCTC
TTCTTCTTCGTCTTCTTCGCCTTCTACAGCTTCGACGACGACATCGGTATGTTCTAGGCA
AACGGTTATGGAAATCGCGACGGCGATCGCGGAAGGGAAAACAGAGATAGCGACGGAGAT
TTTGGCGCGTGTTTCTCAAACGCCTAATCTTGAGAGGAATTCAGAGGAGAAGCTTGTTGA
TTTCATGGTGGCTGCGCTTCGATCGAGGATAGCTTCTCCAGTGACGGAATTGTATGGGAA
GGAGCATTTAATCTCGACTCAATTGCTCTACGAGCTCTCTCCTTGTTTCAAACTCGGTTT
CGAGGCCGCGAATCTCGCCATTCTCGACGCCGCCGATAACAACGACGGTGGAATGATGAT
ACCGCACGTTATCGATTTCGATATCGGAGAAGGTGGACAATACGTTAACCTTCTCCGTAC
ATTATCCACGCGCCGGAATGGTAAAAGTCAGAGTCAGAATTCTCCGGTGGTTAAGATCAC
CGCCGTGGCGAACAACGTTTACGGATGTTTAGTCGATGACGGTGGAGAAGAGAGGTTAAA
AGCCGTCGGAGATTTGTTGAGCCAACTCGGTGATCGACTCGGTATCTCCGTAAGTTTCAA
CGTGGTGACGAGTTTACGACTCGGTGATCTGAATCGTGAATCTCTCGGGTGTGATCCCGA
CGAGACTTTGGCTGTGAACTTAGCTTTCAAGCTTTATCGTGTTCCCGACGAAAGCGTATG
CACGGAGAATCCAAGAGACGAACTTCTCCGGCGCGTGAAGGACTTAAACCGCGCGTGGT
TACTCTAGTGGAGCAAGAAATGAATTCGAATACGGCGCCGTTTTTAGGGAGAGTGAGTGA
GTCATGCGCGTGTTACGGTGCGTTGCTTGAGTCGGTCGAGTCTACGGTTCCTAGTACGAA
TTCCGACCGTGCCAAAGTTGAGGAAGGAATTGGCCGGAAGCTAGTAAACGCGGTGGCGTG
CGAAGGAATCGATCGTATAGAGCGGTGCGAGGTGTTCGGGAAATGGCGAATGCGGATGAG
CATGGCTGGGTTTGAGTTAATGCCATTGAGTGAGAAGATAGCGGAGTCGATGAAGAGTCG
TGGAAACCGAGTCCACCCGGGCTTTACCGTTAAAGAAGATAACGGAGGTGTGTGCTTTGG
TTGGATGGGACGGGCACTCACTGTCGCATCCGCTTGGCGTTAACTTCACACACTCTTTTT
TTTCTTCTTATTATTACCATATTATTATTAATTTTCGAGATTATTCTGATATTATTATCA
TTGTGATTTTCCGTTTCGAAAAGTGTAGGAATCTTATGTAACAAAGAAAAAAAAAAGACT
TTTATGTTTTTCTAATAATAAAAGAAAGAGTGATTGGGTTCAAAAAAAAAAAAAAAAA
AAAAAAAA

FIG. 16G

SRPa8 (10964)

TGCATACAACGCACCGTTTTTCGTAACACGGTTTCGCGAAGCTCTATTTCATTTCTCCTC
GATTTTTGACATGCTTGAGACAATTGTGCCACGAGAAGACGAAGAGAGGATGTTCCTTGA
GATGGAGGTCTTTGGGAGAGAGGCACTGAATGTGATTGCTTGCGAAGGTTGGGAAAGAGT
GGAGAGGCCTGAGACATACAAGCAGTGGCACGTACGGGCTATGAGGTCAGGGTTGGTGCA
GGTTCCATTTGACCCAAGCATTATGAAGACATCGCTGCATAAGGTCCACACATTCTACCA
CAAGGATTTTGTGATCGATCAAGATAACCGGTGGCTCTTGCAAGGCTGGAAGGGAAGAAC
TGTCATGGCTCTTTCTGTTTGGAAACCAGAGTCCAAGGCTTGACCGAGAAATCCTCGTTG
GCATATGAGAGACCATCTCTTGATTTTCTTCCTGTGTAATTCCCAGAGACAGAATTACAG
ATGTAAGAAGAGAATGCTGCACAAAGAACTTGTTCAAAGATAATATTGATGTAAGTCCTG
TTTTATAACTTTCTAGCTGTGTTTTTGTTGTTTCTCAGCTAGATTCTCCTAACGGTATTC
TTGTAGCTAGGGTGATCAGATTGTTTGTATATTGCTAGCAGAGTTAGTTTGTCTAGATTG
TAACACATATAAGAGGAAGCTTAGAGTTTCTATGGTTTAAAGAGAAGTTTTTTCCTTCTC
CAATGTAAAAAAAAAAAAAAAAAA

FIG. 16H

SRPa10 (11261)

AAAAAATGGGAAACCATCACTCTTGATGAACTTATGATCAATCCAGGAGAGACAACGGTC
GTCAACTGCATTCATCGGTTACAATACACTCCTGATGAAACTGTGTCATTAGACTCTCCA
AGAGACACGGTTCTGAAGCTATTCAGAGATATCAATCCTGACCTCTTTGTGTTTGCAGAG
ATTAACGGAATGTACAACTCTCCTTTCTTCATGACGAGGTTCCGAGAAGCGCTTTTTCAT
TACTCTTCACTCTTTGACATGTTTGACACCACAATACACGCAGAGGATGAGTACAAAAAC
AGGTCACTGTTGGAGAGAGAGTTACTTGTGAGAGACGCGATGAGCGTGATTTCCTGCGAG
GGTGCAGAGCGGTTTGCGAGGCCTGAAACCTACAAGCAATGGCGAGTTAGGATTTTGAGA
GCCGGGTTTAAGCCAGCAACTATTAGCAAACAGATCATGAAGGAGGCTAAGGAAATTGTG
AGGAAACGTTACCATAGAGATTTTGTGATCGATAGCGATAACAATTGGATGCTTCAAGGA
TGGAAAGGAAGAGTCATCTATGCTTTTTCTTGCTGGAAACCTGCTGAGAAGTTCACAAAC
AATAATTTAAACATCTGAAAAATGTTACTTCTCAATTACATCATTTTTGTTTCCCAATGG
TTTTGTAGAATATGTTTGATCCCGTGAGTGGATGCAACTCTTTTTTCCTGCAAGTACATA
TTGTATTCAAATCCTTGTGGAAATGATAAATTGTTTAATCAAAAAAAAAAAAAAA

FIG. 16I

SRPa11 (18652)

GCGAATGTTGAGATCTTGGAAGCAATAGCTGGGGAAACCAGAGTCCACATTATCGATTTT
CAGATTGCACAGGGATCACAATACATGTTTTTGATTCAGGAGCTTGCGAAACGCCCTGGT
GGGCCGCCGTTGCTGCGTGTGACGGGTGTGGATGATTCACAGTCCACCTATGCTCGTGGG
GGAGGACTCAGCTTGGTAGGTGAGAGGCTTGCAACTTTGGCGCAGTCATGTGGTGTCCCG
TTTGAGTTTCACGATGCCATCATGTCTGGGTGCAAGGTGCAGCGGGAACATCTCGGGTTG
GAACCTGGCTTTGCTGTTGTTGTGAACTTCCCATATGTATTACACCACATGCCAGACGAG
AGCGTAAGTGTTGAAAAATACAGAGACAGGCTGCTGCATCTGATCAAGAGCCTCTCCCCA
AAACTGGTTACTCTAGTAGAGCAAGAATCCAACACAAACACCTCGCCATTGGTGTCACGG
TTTGTGGAAACACTGGATTACTACACAGCGATGTTTGAGTCGATAGATGCAGCACGGCCA
CGGGATGATAAGCAGAGAATCAGCGCAGAACAACACTGTGTAGCAAGAGACATAGTGAAC
ATGATAGCATGTGAGGAGTCAGAGAGAGTAGAGAGACACGAGGTACTGGGGAAATGGAGG
GTCAGAATGATGATGGCTGGGTTCACGGGTTGGCCGGTCAGCACATCTGCAGCGTTTGCA
GCGAGTGAGATGCTGAAAGCTTATGACAAAAACTACAAACTGGGAGGCCATGAAGGAGCG
CTCTACCTCTTCTGGAAGAGACGACCCATGGCTACATGTTCCGTGTGGAAGCCAAACCCA
AACTATATTGGGTAAGTTATAGTGATGATGGTTACTTGAGTGGATAAAGAAGAGCACAAC
AAAAACACATCTGTCGCTGTAAATTTTTTAGGATGTGCAATGATGTTTTAAGTTGTAACA
CAACCTAAGTTATATATGTATACAAACCAAACCTGGTGGTTGTTTTTCTCTTGTAAATTG
TCATGTGGTTGTGGGTGGGAAGCTAGTAATGAAATATAACCAAAACATTGATTAGGTCAA
AAAAAAAAAAAAA

FIG. 16J

SRPa12 (23196)*

TCTTACTCAAGGTTCTTCTTTGTCATCTTGTTGCCGAATCCACAAAGAGGAGAATAAAGA
TTCGACCTTTATTAGATATTAACGACTCTGGATTTTTGGGTTTTTGGAGTTGGATCCACA
TGGGTTCTTATCCGGATGGATTCCCTGGATCCATGGACGAGTTGGATTTCAATAAGGACT
TTGATTTGCCTCCCTCCTCAAACCAAACCTTAGGTTTAGCTAATGGGTTCTATTTAGATG
ACTTAGATTTCTCATCCTTGGATCCTCCAGAGGCATATCCCTCCCAGAACAACAACAACA
ACAACATCAACAACAAAGCTGTAGCAGGAGATCTGTTATCATCTTCATCTGATGACGCTG
ATTTCTCTGATTCTGTTTTGAAGTATATAAGCCAAGTTCTTATGGAAGAGGATATGGAAG
AGAAGCCTTGTATGTTTCATGATGCTTTGGCTCTTCAAGCTGCTGAGAAATCTCTCTATG
AGGCTCTTGGTGAGAAAGACCCTTCTTCGTCTTCTGCTTCTTCTGTGGATCATCCTGAGA
GATTGGCTAGTCATAGCCCTGACGGTTCTTGTTCAGGTGGTGCTTTTAGTGATTACGCTA
GCACCACTACCACTACTTCCTCTGATTCTCACTGGAGTGTTGATGGTTTGGAGAATAGAC
CTTCTTGGTTACATACACCTATGCCGAGTAATTTTGTTTTCCAGTCTACTTCTAGGTCCA
ACAGTGTCACCGGTGGTGGTGGTGGTGGTAATAGTGCGGTTTACGGTTCAGGTTTTGGCG
ATGATTTGGTTTCGAATATGTTTAAAGATGATGAATTGGCTATGCAGTTCAAGAAAGGGG
TTGAGGAAGCTAGTAAGTTCCTTCCTAAGTCTTCTCAGCTCTTTATTGATGTGGATAGTT
ACATCCCTATGAATTCTGGTTCCAAGGAAAATGGTTCTGAGGTTTTTGTTAAGACGGAGA
AGAAAGATGAGACAGAGCATCATCATCATCATAGCTATGCACCACCACCCAACAGATTAA
CTGGTAAGAAAAGCCATTGGCGCGACGAAGATGAAGATTTCGTTGAAGAAAGAAGTAACA
AGCAATCAGCTGTTTATGTTGAGGAAAGCGAGCTTTCTGAAATGTTTGATAACATGTTCC
TATGTGGCCCTGGGAAACCTGTATGCATTCTTAACCAGAACTTTCCTACAGAATCCGCTA
AAGTCGTGACCGCACAGTCAAATGGAGCAAAGATTCGTGGGAAGAAATCAACTTCTACTA
GTCATAGTAACGATTCTAAGAAAGAAACTGCTGATTTGAGGACTCTTTTGGTGTTATGTG
CACAAGCTGTATCAGTGGATGATCGTAGAACCGCCAACGTTTAGCTAAGGCAGATACGAG
AGCATTCTTCGCCTCTAGGCAATGGTTCAGAGCGGTTGGCTCATTATTTTGCAAATAGTC
TTGAAGCACGCTTAGCTGGGACCGGTACACAGATCTACACCGCTTTATCTTCGAAGAAAA
CGTCTGCAGCAGACATGTTGAAGGCTTACCAGACATACATGTCGGTCTGCCCTTTCAAGA
AAGCTGCTATCATATTTGCTAACCACAGCATGATGCGTTTCACTGCAAACGCCAACACGA
TCCACATAATAGATTTCGGAATATCTTACGGTTTTCAGTGGCCTGCTCTGATTCATCGCC
TCTCGCTCAGCAGACCTGGTGGTTCGCCTAAGCTTCGAATTACCGGTNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNGAGTTCAGGAGACAGGTCATCGCTTGGCTCGATACT
GTCAGCGACACAATGTTCCGTTTGAGTACAACGCAATTGCTCAGAAATGGGGAAACGATC
CAAGTCGAAGACTTAAAGCTTCGACAAGGAGAGTATGTGGTTGTGAACTCTTTGTTCCGT
TTCAGGAACCTTCTAGATGAGACCGTTCTGGTAAACAGCCCGAGAGATGCAGTTTTGAAG
CTGATAAGAAAAATAAACCCGAATGTCTTCATTCCAGCGATCTTAAGCGGGAATTACAAC
GCGCCATTCTTTGTCACGAGGTTCAGAGAAGCGTTGTTTCATTACTCGGCTGTGTTTGAT
ATGTGTGACTCGAAGCTAGCTAGGGAAGACGAGATGAGGCTGATGTATGTGTTTGAGTTT
TATGGGAGAGAGATTGTGAATGTTGTGGCTTCTGAAGGAACAGAGAGAGTGGAGAGCCGA
GAGACATATAAGCAGTGGCAGGCGAGACTGATCCGAGCCGGATTTAGACAGCTTCCGCTT
GAGAAGGAACTGATGCAGAATCTGAAGTTGAAAATCGAAAACGGGTACGATAAAAACTTC
GATGTTGATCAAAACGGTAACTGGTTACTTCAAGGGTGGAAAGGTAGAATCGTGTATGCT
TCATCTCTATGGGTTCCTTCGTCTTCATAGATGTTGTTTCTTACGTTCTAAGCGACTGGG
ATTTATGTAGGGCTTTTCTGTTGATAGTCTCTCGCCAACACGAGTGGATTAAGTTCAGAG
TTAGGGTTCTTGAACACTAGAATGTTGTTATATTATGCTTGTGACATAGCGTGTGTAAGA
GTGTAGCCTAAGAGATATAGTACTCATTGCATGATCTTTTGCTATATGTTNCATGT

FIG. 16K

SRPd1

TCTGCAGACAATTTTNAGGAGGCCAATACCATGCTATTGGAAATTTCAGAACTG
TCCACACCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTACTTCTCAGAGGN
AATGTCGGNNAGATTAGTTAGCTCCTGCTTAGGAATCTATGCTTCTCTTCCNGC
AACAGTGGTGCCTCCTCATGGTCAGAAAGTGGCCTCA

FIG. 16L

SRPg1

TCAACTGAGAATCTAGAAGATGCCAACAAGATGCTTCTGGAGATTTCTCAGTTA
TCAACACCGTTCNNCACTTCAGCACAGCGTGTGGCAGCATATTTCTCAGAAGCC
ATATCAGCAAGGTTGGTGAGTTCATGTCTAGGGATATACGCAACTTTGCCACAC
ACACACCAAAGCCACAAGGTAGCTTCAGCTTTTCAAGTGTTCAATGGTATTAGT
CCTTTAGTGGAGTTCTCACACTTCACAGCAAACCAAGCAATTCAAGAAGCCTTC
GAAAGAGAAGAGAGGGTGCACATCATAGATCTTGATATAATGCAAGGGTTG

FIG. 16M

SRPp1

TCTGCAGACAACTTTGAAGAAGCCAATACAATACTGCCTCAGATCACAGAACTC
TCCACCCCCTATNGCAACTCGGTGCAACGAGTGGCTGCCTATNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNTGCATAGGAATGTATTCTCCTCTCCCTCCT
ATTCACATGTCCCAGAGCCAGAAAATTGTGAAT

FIG. 17A

Partial DNA sequence of *ZCARECROW* gene

GATATCAGCATCATCAATTTTAAATGTAAGTTGGCAAAAGATCATGAGGGTTCTCATAGT
AATTTGGCCACAAGGTATGACACTGTCTCAATTGAGCAATCTAGTAGAGAAACTGATCCA
TCATATATTGCTCATATTGAAAGTGAAAAAGATATGCTCAAGAACCTAGTAGAGAAGCTA
AAAATTGAAAAATCTAGCTCTACTAGAAAAATATGATAGGTTGCCTGTTTCTCATGAAAA
TTTATTAGATAATCATATCATGGCTAGATGTCGCTCATGAGGTTGTTCTTGCTAGTTTAG
ATTCCTGTGGGCATTCATCTCTTTTAGATGCACTAACATGATAGGAAGTTTCTAATCTGG
TGCTTCACAATTCTGGTGATTCATGCTTCCTTCATTGCAATTGATATTGATGCTTGATTC
ATGCTTCAGTCACTTTGTGCGTTTAATTGGTATTGTATGTATCACTAGATTGTAGGGTGT
CTGCAACTAGTGTTTCACCATGTGGTTTTTTAGTATCATTCGTATTAGTTTCTAACTTTC
TATTGATATATTAAAGTGATAACTAGTTTTAGAAATATTCTCTTGTGCCATTAATGCTAC
AACTTGTTTTTAGCGTGTACGTTAGCATTATAATATTTCCTTATTATGAAAGCGGAAGAG
AAACGCGCCCAACCAGAGCATCCACGTCGTCTCATTTCACCTTCATCGTTGGATCATAGA
TGAGCGGTCCACGGTGAACTCCGTTTGCCTGCAAAACCACGTCCTCTACGCGCTGTTAAG
TAGCTTCTAGAAACATCACGATGTGTCCCGTCCATTCCTTTAGGAGGAGCCGGATCCGGC
GCCGCAGTCGCCCAAGGTCCCGACCGCCGCGGCCTCGGCCGCCGCCGCCAAGGAGCGGAA
GGAGGTGCAGCGGCGGAAGCAGCGCGACGAGGAGGGCCTCCACCTGCTGAGTGCTGACGC
TGCTGCTGCAGTGCGCGGAGGCCGTGAACGCGGACAACCTCGACGACGCGCACCAGACGC
TGCTGGAGATCGCGGAGCTGGCCACGCCGTTCGGCACCTCGACCCAGCGCGTGGCCGCCT
ACTTCGCGGAGGCCATGTCGGCGCGCGTCGTCAGCTCCTGCCTAGGCCTGTACGCGCCGC
TGCCGCCGGGCTCCCCCGCCGCGGCGCGCCTCCACGGCCGCGTGGCCGCCGCGTTCCAGG
TGTTCAACGGCATCAGCCCCTTCGTCAAGTTCTCGCACTTCACCGCCAACCAGGCCATCC
AGGAGGCGTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACATCATGCAGGGGC
TGCAGTGGCCGGGCCTCTTCCACATCCTTGTCTCCCGCCCCGGCGGCCCGCCCAGGGTCA
GGCTCACCGGCCTGGGGGCGTCCATGGACGCGCTCGAGGCGACGGGGAAGCGCCTCTCCG
ACTTCGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTCGCCGAGAAGGCCGGCA
ACGTTGACCCGCAGAAGCTGGGCGTCACGCGGCGGGAGGCCGTCGCCGTCCACTGGCCGC
ACCACTCGCTTTACGACGTCATCGGCTCCGACTCCAACACGCTCTGGCTCATCCAAAGGT
CCTCCATTTTCCTTCTCTGCCTTTCTTCCATGTCAAATCTTGATGCAATCATGACCACTT
TTCAGCTGCTGACATTGGATAATGTGAGCTTTACGGCAAGCATCAAGTCGTGGTAGTACA
TCCATTACAGCTATTTCTAAAATATTCTTCGGAGGTTTCCTGCTCATAGTAAAAAAAAT
CGCGTTTTGAAGCTCAAAAGGCGATTTCTTCCGAGGTTTGCTGTTGAGCGCTATTTTGGA
AACCCCATTTTCTCAATTGATTTTTATTTTTTAAAGAAAAATTAGTTCATTTTTCTCTTG
TGAAATGGAGTCCCAAACTAACCCTAATATTAAAAAAAACGCGCTTTGGAGCTCAAAACG
CTCGTTGTTATGACCAACCAGCTTTATAGGTTTAAAAAGGTTGAATCTTGACAATGCTTT
TGAAAAGGTTGAATCTTGACAATGCTTTTGAGATGATACTGTAGTGTAGTCTGTAGTGGA
GCATCCTCCATGGTCTTTGGTGATCGAGAATTCCTGCAGCCCGGGGGATCC

FIG. 17B

Partial amino acid sequence of ZCARECROW protein

YQHHQFXMXVGKRSXGFSXXFGHKVXHCLNXAIXXRNXSIIYCSYXKXKRYAQEPSREAK
NXKIXLYXKNMIGCLFLMKIYXIIISWLDVAHEVVLASLDSCGHSSLLDALTXXEVSNLV
LHNSGDSCFLHCNXYXCLIHASVTLCVXLVLYVSLDCRVSATSVSPCGFLVSFVLVSNFL
LIYXSDNXFXKYSLVPLMLQLVFSVYVSIIIFPYYESGRETRPTRASTSSHFTFIVGSXM
SGPRXTPFACKTTSSTRCXVASRNITMCPVHSFRRSRIRRRSRPRSRPPRPRPPPPRSGR
RCSGGSSATRRASTCXVLTLLLQCAEAVNADNLDDAHQTLLEIAELATPFGTSTQRVAAY
FAEAMSARVVSSCLGLYAPLPPGSPAAARLHGRVAAAFQVFNGISPFVKFSHFTANQAIQ
EAFEREERVHIIDLDIMQGLQWPGLFHILVSRPGGPPRVRLTGLGASMDALEATGKRLSD
FADTLGLPFEFCAVAEKAGNVDPQKLGVTRREAVAVHWPHHSLYDVIGSDSNTLWLIQRS
SIFLLCLSSMSNLDAIMTTFQLLTLDNVSFTASIKSWXYIHYSYFXNILRRFPAHSKKKS
RFEAQKAISSEVCCXALFWKPHFLNXFLFFKEKLVHFSLVKWSPKLTLILKKTRFGAQNA
RCYDQPALXVXKGXILTMLLKRLNLDNAFEMILXCSLXWSILHGLWXSRIPAARGI

FIG. 18

```
                                                                  349
          302
SCR       SADNLEEANKLLLEISQLSTPYGTSAQRVAAYFSEAMSARLLNSCLGI
SRPd1     SADNFxEANTMLLEISELSTPxxxxxxxxxxYFSxxMSxRLVSSxLxI
SRPg1     STENLEDANKMLLEISQLSTGxxxxxxxxxxxxxxxxxxxxxxSCLGI
SRPp1     SADNFEEANTILPQITELSTPYxNSVGRVAAYxxxxxxxxxxxxCIGM

                                                                  396
          350
SCR       YAALPSRWMPQTH-SLKMVSAFQVFNGISPLVKFSHFTANQAIQEAFE
SRPd1     YASLPATVVP--PHGQKVAS
SRPg1     YATLP-----HTHQSHKVASAFQVFNGISPLVEFSHFTANQAIQEAFE
SRPp1     YSPLPPIxMSQ---SQKIVN

          397           412
SCR       KEDSVHIIDLDIMQGL
SRPg1     REERVHIIDLDIMQGL
```

FIG. 19

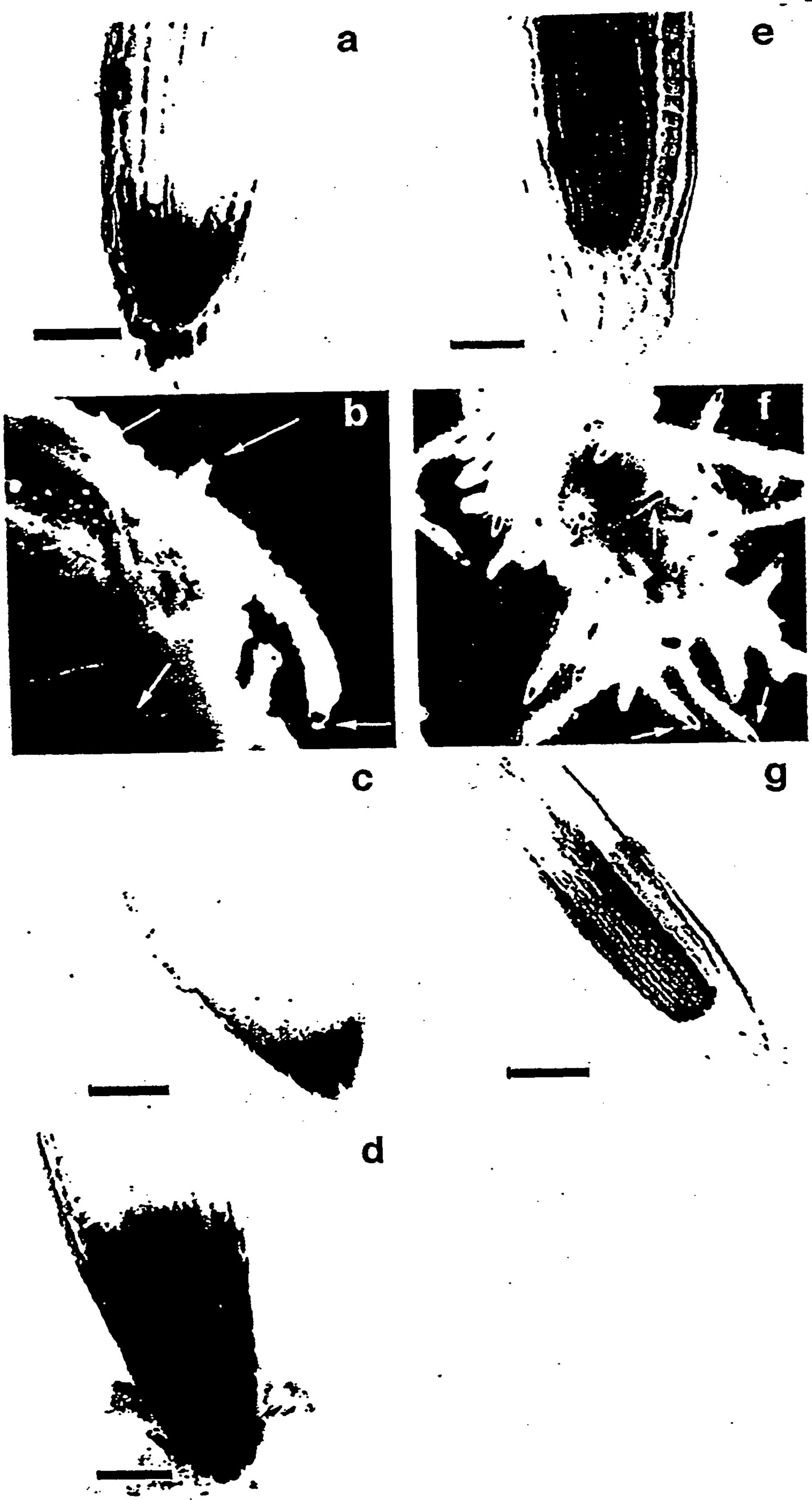


FIG. 20

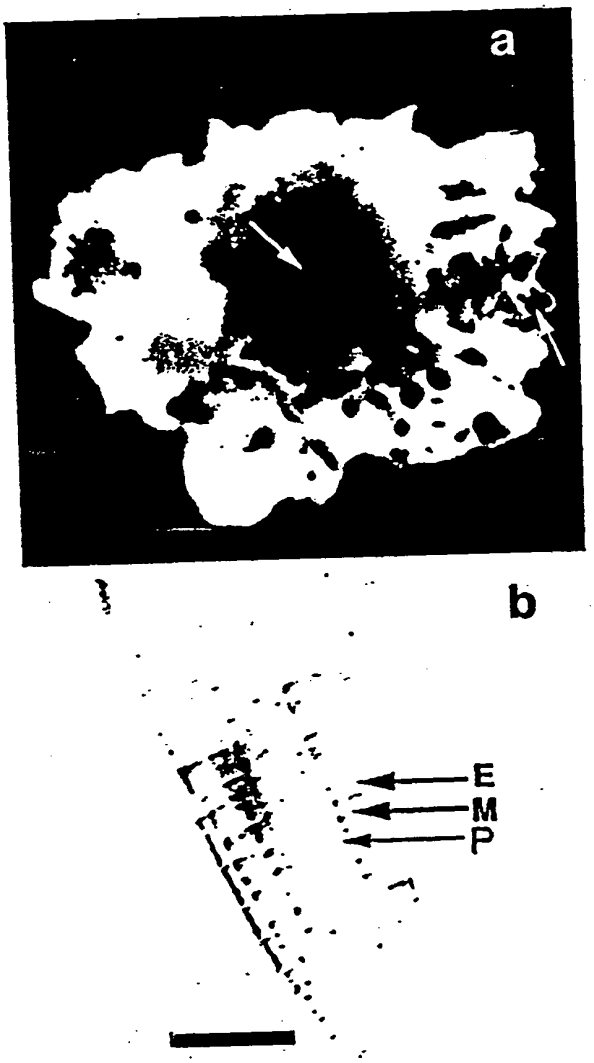
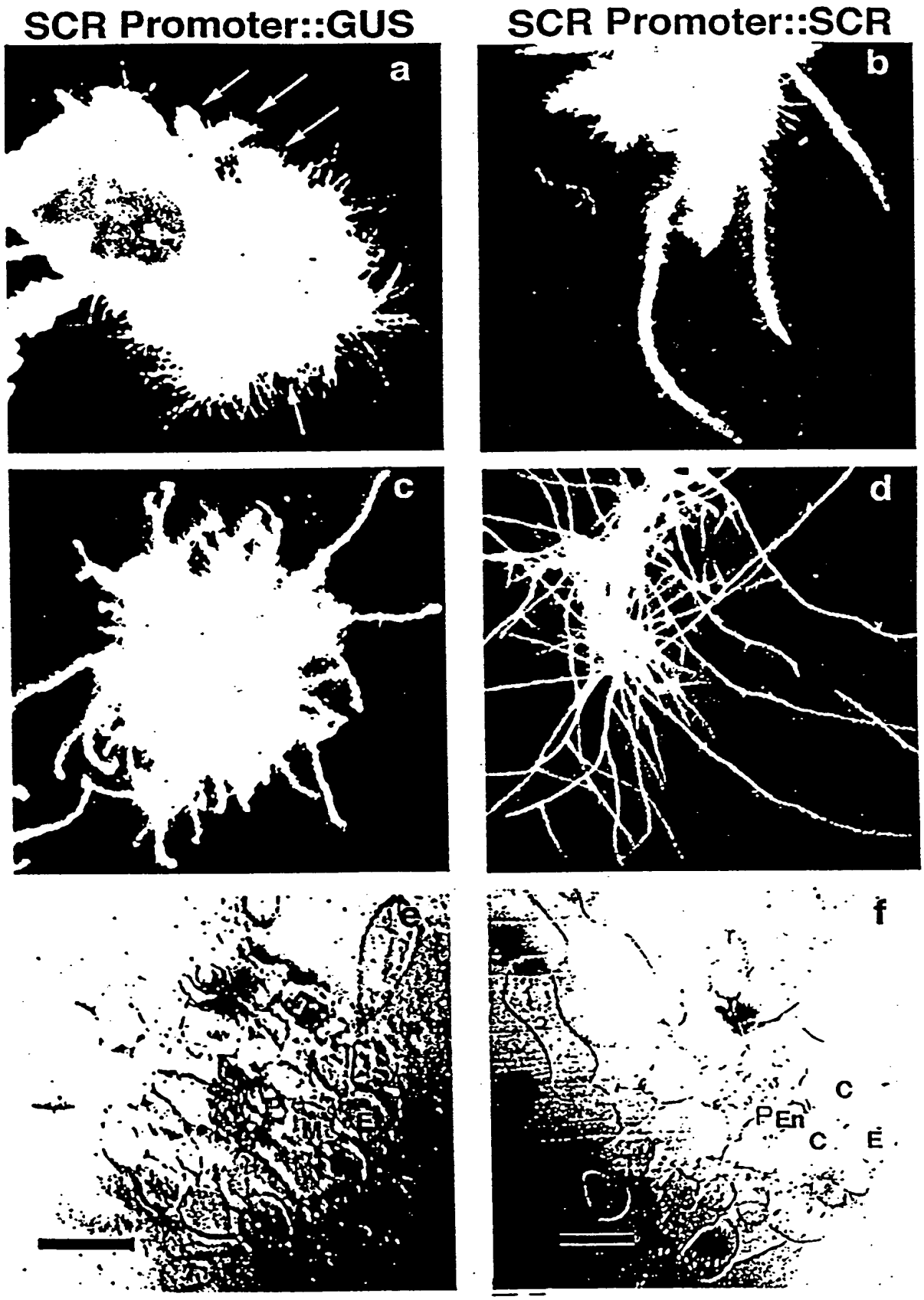


FIG. 21



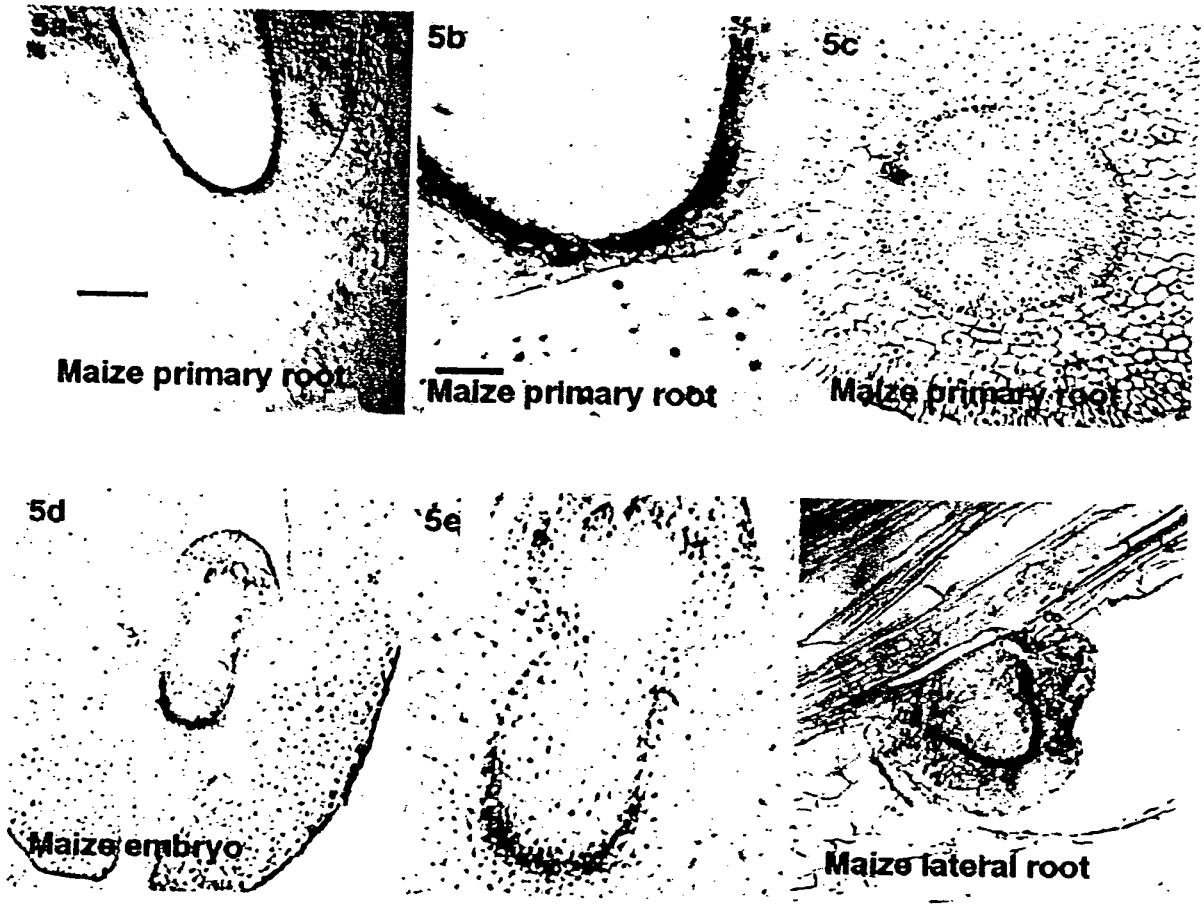
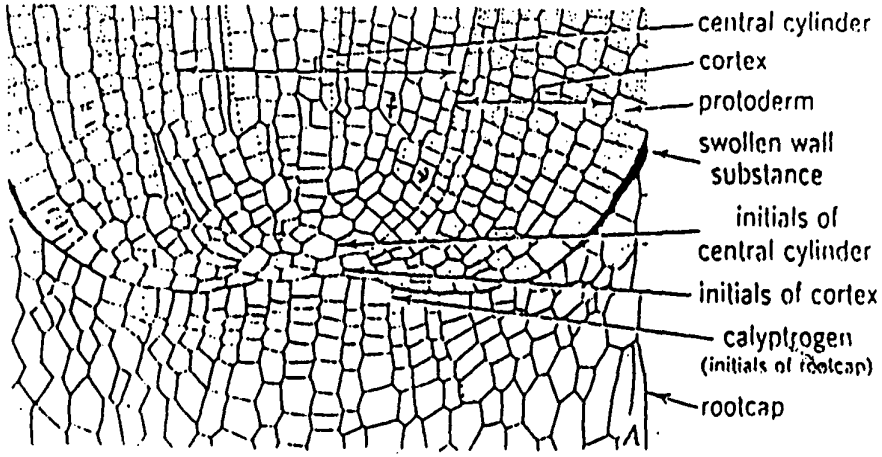
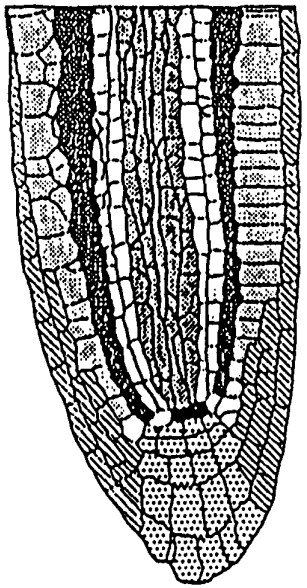


Fig. 22

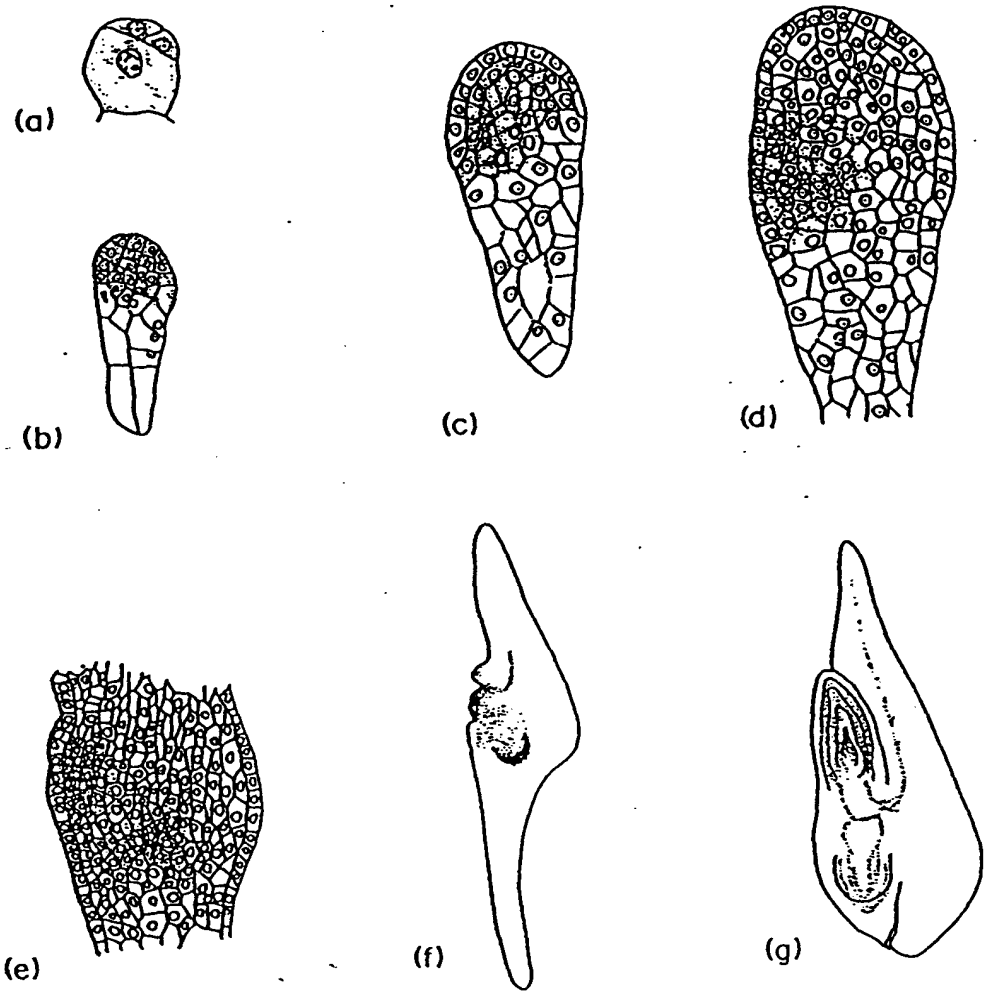


A. monocotyledonous closed-type (Zea).



B. dicotyledonous closed-type (Arabidopsis).

The schematic representation of the root apical meristems of maize (A..) And Arabidopsis (B.). Both show a type of a closed meristem in which all files of cells coverage onto a pole at the root apex, making the boundary between the root proper and the root cap discrete.



Embryo development in maize. (a) Three-celled embryo showing first division of terminal cell. (b)-(c) Embryos showing embryo proper and suspensor. (d)-(e) Embryos showing the initial development of shoot and root apical meristems. (f)-(g) Embryos showing the elaborate organization of shoot and root apical meristems.

Fig. 24

```
      ctgctagctcagcctactcactccactcaactcacccccaactccactccgctcccgagc    60
      ccggactgactgactgactgtggtggtggtggtgcatcagcagcccgcgcggcgccaaaa   120
      cacgcaaactgctccctccctcactcacccctatcccccgcgctgggtcgcccgatcgcc   180
      atgcgcgcggcggcttcctcttggcgtttctagatgggctcctcctcctccctcctcttc   240
      tcctcgtcctcctccgccgcatccaccgcccccccactcctttccccactctcATGCCACC   300
  1                                                       M  P  P
      GCCACCGCCTCCGCCTCCTCTCACTCCTTATTGCCGCCGCTGCCCTCCCCCACACCTCCC   360
  4     P  P  P  P  P  P  L  T  P  Y  C  R  R  C  P  P  P  H  L  P
      TCCGCCTCCTCCTTCTTCCCCAAACCACTTCCTCCTCCACTACCTCCATCAGCTAGACCA   420
 24     P  P  P  P  S  S  P  N  H  F  L  L  H  Y  L  H  Q  L  D  H
      CCAAGAAGCCGCCGCCGCCGCCATGGTCCGCAAGCGCCCCGCGTCCGACATGGACCTCCC   480
 44     Q  E  A  A  A  A  A  M  V  R  K  R  P  A  S  D  M  D  L  P
      GCCGCCGCGCCGCCACGTCACGGGCGACCTCTCCGACGTCACGGCGGCCGCTGCCGCCGG   540
 64     P  P  R  R  H  V  T  G  D  L  S  D  V  T  A  A  A  A  A  G
      TGTTGGTGGTAGTGGCGCGCCGTCCTCCGCCAGCGCGCAGCTGCCCGCGCTGCCCACCCA   600
 84     V  G  G  S  G  A  P  S  S  A  S  A  Q  L  P  A  L  P  T  Q
      GCTCCACCAGCTGCCCCCCGCGTTCCAGCACCACGCGCCGGAGGTGGACGTGCCCGCGCA   660
104     L  H  Q  L  P  P  A  F  Q  H  H  A  P  E  V  D  V  P  A  H
      CCCGGCCCCGGCCGCCCACGCGCAGGCGGGCGGCGAGGCAACCGCGTCCACGACCGCGTG   720
124     P  A  P  A  A  H  A  Q  A  G  G  E  A  T  A  S  T  T  A  W
      GGTGGACGGCATCATCCGCGACATCATCGGGAGCAGCGGCGGCGCCGCGGTCTCCATCAC   780
144     V  D  G  I  I  R  D  I  I  G  S  S  G  G  A  A  V  S  I  T
      GCAGCTCATCCACAACGTCCGCGAGATCATCCACCCCTGCAACCCCGGCCTCGCGTCGCT   840
164     Q  L  I  H  N  V  R  E  I  I  H  P  C  N  P  G  L  A  S  L
      CCTGGAGCTCCGCCTCCGCTCCCTCCTCGCAGCCGACCCGGCCCCACTGCCGCCGCCGCC   900
184     L  E  L  R  L  R  S  L  L  A  A  D  P  A  P  L  P  P  P  P
      GCAGCCGCAGCAGCATGCTCTCCTGCACGGCGCTCCGGCCGCCGCTCCCGCGGGGCTGAC   960
204     Q  P  Q  Q  H  A  L  L  H  G  A  P  A  A  A  P  A  G  L  T
      GCTCCCTCCCCCGCCACCGCTTCCGGACAAGCGCCGCCACGAGCATCCACCGCCGTGCCA  1020
224     L  P  P  P  P  P  L  P  D  K  R  R  H  E  H  P  P  P  C  Q
      GCAGCAACAGCAGGAGGAACCGCATCCGGCGCCGCAGTCGCCCAAGGCCCCGACCGCGGA  1080
244     Q  Q  Q  Q  E  E  P  H  P  A  P  Q  S  P  K  A  P  T  A  E
      AGAGACCGCAGCGGCGGCCGCCGCCGCACAAGCAGCAGCTGCTGCGGCCGCCAAGGAGCG  1140
264     E  T  A  A  A  A  A  A  A  A  Q  A  A  A  A  A  A  A  K  E  R
      GAAGGAGGAGCAGCGGCGGAAGCAGCGCGACGAGGAGGGCCTCCACCTGCTGACGCTGCT  1200
284     K  E  E  Q  R  R  K  Q  R  D  E  E  G  L  H  L  L  T  L  L
      GCTGCAGTGCGCCGAGGCCGTGAACGCGGACAACCTGGACGACGCGCACCAGACGCTGCT  1260
304     L  Q  C  A  E  A  V  N  A  D  N  L  D  D  A  H  Q  T  L  L
      GGAGATCGCGGAGCTAGCGACGCCGTTCGGCACCTCGACGCAGCGCGTGGCCGCCTACTT  1320
324     E  I  A  E  L  A  T  P  F  G  T  S  T  Q  R  V  A  A  Y  F
      CGCGGAGGCCATGTCGGCGCGGCTCGTCAGCTCCTGCCTGGGCCTGTACGCGCCGCTGCC  1380
344     A  E  A  M  S  A  R  L  V  S  S  C  L  G  L  Y  A  P  L  P
      GCCGGGCTCCCCCGCCGCGGCGCGCCTCCACGGCCGCGTCGCCGCCGCGTTCCAGGTGTT  1440
364     P  G  S  P  A  A  A  R  L  H  G  R  V  A  A  A  F  Q  V  F
      CAACGGCATCAGCCCCTTCGTCAAGTTCTCGCACTTCACCGCCAACCAGGCCATCCAGGA  1500
384     N  G  I  S  P  F  V  K  F  S  H  F  T  A  N  Q  A  I  Q  E
      GGCGTTCGAGCGGGAGGAGCGCGTGCACATCATCGACCTCGACATCATGCAGGGGCTGCA  1560
404     A  F  E  R  E  E  R  V  H  I  I  D  L  D  I  M  Q  G  L  Q
      GTGGCCGGGGCTCTTCCACATCCTTGCCTCCCGCCCCGGGGGCCCGCCCAGGGTGAGGCT  1620
424     W  P  G  L  F  H  I  L  A  S  R  P  G  G  P  P  R  V  R  L
      CACCGGCCTCGGGGCGTCCATGGAGGCGCTCGAGGCCACGGGGAAGCGCCTCTCCGATTT  1680
444     T  G  L  G  A  S  M  E  A  L  E  A  T  G  K  R  L  S  D  F
      CGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTCGCCGAGAAGGCCGGCAATGT  1740
464     A  D  T  L  G  L  P  F  E  F  C  A  V  A  E  K  A  G  N  V
```

Fig. 25A

```
     TGACCCGGAGAAGCTAGGGGTCACGAGGCGGGAGGCCGTCGCCGTCCACTGGCTGCACCA  1800
484    D  P  E  K  L  G  V  T  R  R  E  A  V  A  V  H  W  L  H  H
     CTCGCTCTACGACGTCACTGGCTCCGACTCCAACACGCTCTGGCTCATCCAAAGgtagga  1860
504    S  L  Y  D  V  T  G  S  D  S  N  T  L  W  L  I  Q  R
     aggagtacaccatctctcgatcctgacttccttgctaccatgtcaaatcttgatgcaatc  1920
     atggccacttttcagctactaacactttagtttagccaatgcgacatccagtacaactaa  1980
     tctaaaaaaataatcttcagaggtttcctagtaaaaaaaccgcgtttttggagctcaaaa  2040
     agcttgtcattatgaccaaccaactttctaggcttaaaaaggttgaatcttggcaatgct  2100
     tttgagacgatgctgtactgaagtactggtagagagagtatcctccatggcctttgttga  2160
     tcccagaaccacaaaagatagtatttcgctcgcatttggttagtggaggtgttctgatca  2220
     tcacttggaggatggagctgaaagttcctatcatcatgaccaactttccatggcaaaagg  2280
     tttctagttccaagtggcaggacgatgattactgagtgactgaatggagtaactgtcatc  2340
     ttctaccactaaccatcatttattaatacataaatcatcatccggagcctaaactcagaa  2400
     aggctaatcaaaagtgcaatctttctcaaatggctgccatatgccagtggtacatgcctg  2460
     gccattgtacttttcggtgaaccatctcgtctcaagcatgagatgaaggcctgaactgc  2520
     aatgtccttgatttgatgcaaccattattagaagaaacgctaagcgatgccggtcctggc  2580
     aagggcaatgccatatcgtcagacagacagggattcggaatcgaatggctagctggtgac  2640
     aaatcgcacggggattaataaactacattggtcattgattccatcccccacacacctgca  2700
     gGCTGGCCCCCAAGGTGGTGACAATGGTGGAGCAGGACCTGAGCCACTCGGGCTCCTTCC  2760
522    L  A  P  K  V  V  T  M  V  E  Q  D  L  S  H  S  G  S  F
     TGGCGCGCTTCGTGGAGGCCATCCACTACTACTCGGCGCTGTTCGACTCGCTGGACGCGA  2820
541  L  A  R  F  V  E  A  I  H  Y  Y  S  A  L  F  D  S  L  D  A
     GCTACGGCGAGGACAGCCCCGAGCGGCACGTCGTGGAGCAGCAGCTGCTGTCGCGGGAGA  2880
561  S  Y  G  E  D  S  P  E  R  H  V  V  E  Q  Q  L  L  S  R  E
     TCCGCAACGTGCTGGCCGTGGGCGGGCCGGCCCGCACCGGCGACGTCAAGTTCGGCAGCT  2940
581  I  R  N  V  L  A  V  G  G  P  A  R  T  G  D  V  K  F  G  S
     GGCGCGAGAAGCTGGCGCAGTCCGGGTTCCGCGCCGCCTCGCTCGCCGGCAGCGCCGCGG  3000
601  W  R  E  K  L  A  Q  S  G  F  R  A  A  S  L  A  G  S  A  A
     CGCAGGCGTCCCTGCTGCTCGGCATGTTCCCCTCCGACGGGTACACGCTGGTGGAGGAGA  3060
621  A  Q  A  S  L  L  L  G  M  F  P  S  D  G  Y  T  L  V  E  E
     ACGGCGCGCTGAAGCTCGGGTGGAAGGACCTCTGCCTGCTCACCGCGTCGGCCTGGCGCC  3120
641  N  G  A  L  K  L  G  W  K  D  L  C  L  L  T  A  S  A  W  R
     CCATCCAGGTGCCGCCGTGCCGTTGAtgagacctctgcctgctcctgcttgcgttgagag  3180
661  P  I  Q  V  P  P  C  R  *
     gccgccactccacttgttttgcatctgtagctgctcggtttggtcatcagctgggagata  3240
     agaaaagcggaaacgtactaattgctctggagtagatccatccattcacagtgatagtta  3300
     ctgatgtactaagctttaattagttcaatgctagatcgttcttgttcaggtgtcgatcgc  3360
     gtatccttgtccttggtctccttttcattttggtgctttgtctagtcgctttcccgacta  3420
     atgccgtgctcttcatgcgcgttctagtgaagattcttgccgagaatattagcatagttt  3480
     tcatgtaaagtagccatcaagcaagtatta  3510
```

Nucleotide and deduced amino acid sequence of the maize *SCARECROW*. Amino acid numbers are shown to the left; nucleotides are numbered on the right. Forward and reverse primers tested are underlined (J1050F and J1450R).

Fig. 25B

```
                *                    *** *      **
Zm SCR   MPPPPPPPPL TPYCRRCPPP HLPPPPPSSP NHFLLHYLHQ LDHQEAAAAA   50
At SCR   MAES------ GDFNGGQPPP HSPLRTTSSG SSSSNN--RG PPPPPPPPLV   42

                ***** ** *    *             *           *      **  * *
Zm SCR   MVRKRPASDM DLPP---PRR HVTGDLSDVT AAAAAGVGGS GAPS-SASAQ   96
At SCR   MVRKRLASEM SSNPDYNNSS RPPRRVSHLL DSNYNTVTPQ QPPSLTAAAT   92

                   *                                  *       ** * *
Zm SCR   LPALPTQLHQ LP--PAFQHH APEVDVPAHP APAAH-AQAG GEATASTTAW   143
At SCR   VSSQPNPPLS VCGFSGLPVF PSDRGGRNVM MSVQPMDQDS SSSSASPTVW   142

                ** **** *  **    ***  *** *** **  **** *  * ** *****
Zm SCR   VDGIIRDIIG SSGGAAVSIT QLIHNVREII HPCNPGLASL LELRLRSLLA   193
At SCR   VDAIIRDLIH SS--TSVSIP QLIQNVRDII FPCNPNLGAL LEYRLRSLML   190

                 **      *  **    *               *             * **
Zm SCR   ADPAPLPPPP QPQQHALLHG APAAAPAGLT LPPPPPLPDK RRHEHPPPCQ   243
At SCR   LDPSS-SSDP SPQTFEPLYQ ISNNPSP--- -PQQQQQHQQ QQQQHKPPPP   235

                  ** *          *  *    *   * *    * *  ** *** *   *
Zm SCR   QQQQEEPHPA PQSPKAPTAE ETAAAAAAAQ AAAAAAAKER KEEQRRKQRD   293
At SCR   PIQQQERENS STDA-PPQPE TVTATVPAVQ TNTAEALRER KEEIKRQKQD   284

                **********  ******* ** **  *   ** **  * ** * ** *******
Zm SCR   EEGLHLLTLL LQCAEAVNAD NLDDAHQTLL EIAELATPFG TSTQRVAAYF   343
At SCR   EEGLHLLTLL LQCAEAVSAD NLEEANKLLL EISQLSTPYG TSAQRVAAYF   334

                 *******   **** ** **                  ***** ***** ****
Zm SCR   AEAMSARLVS SCLGLYAPLP PGSPAAARLH GRVAAAFQVF NGISPFVKFS   393
At SCR   SEAMSARLLN SCLGIYAALP SRWMPQTH-S LKMVSAFQVF NGISPLVKFS   383

                **********  *** *  *** **********  **********  ****** ***
Zm SCR   HFTANQAIQE AFEREERVHI IDLDIMQGLQ WPGLFHILAS RPGGPPRVRL   443
At SCR   HFTANQAIQE AFEKEDSVHI IDLDIMQGLQ WPGLFHILAS RPGGPPHVRL   433

                **** *****  *********  * ******* *  *** **   * * * *  *
Zm SCR   TGLGASMEAL EATGKRLSDF ADTLGLPFEF CAVAEKAGNV DPEKLGVTRR   493
At SCR   TGLGTSMEAL QATGKRLSDF TDKLGLPFEF CPLAEKVGNL DTERLNVRKR   483

                ******** * *********   **** **** ***** **** *** **** *
Zm SCR   EAVAVHWLHH SLYDVTGSDS NTLWLIQRLA PKVVTMVEQD LSHSGSFLAR   543
At SCR   EAVAVHWLQH SLYDVTGSDA HTLWLLQRLA PKVVTVVEQD LSHAGSFLGR   533

                **********  ***** **** * * ******  ***** **** ******* *
Zm SCR   FVEAIHYYSA LFDSLDASYG EDSPERHVVE QQLLSREIRN VLAVGGPART   593
At SCR   FVEAIHYYSA LFDSLGASYG EESEERHVVE QQLLSKEIRN VLAVGGPSRS   583

                * *** **** *  * **    **** ** **  ********* *****  **
Zm SCR   GDVKFGSWRE KLAQSGFRAA SLAGSAAAQA SLLLGMFPSD GYTLVEENGA   643
At SCR   GEVKFESWRE KMQQCGFKGI SLAGNAATQA TLLLGMFPSD GYTLVDDNGT   633

                ******** * ******  *
Zm SCR   LKLGWKDLCL LTASAWRPIQ VPPCR   668
At SCR   LKLGWKDLSL LTASAWTPR- ----S   653
```

Fig. 26A

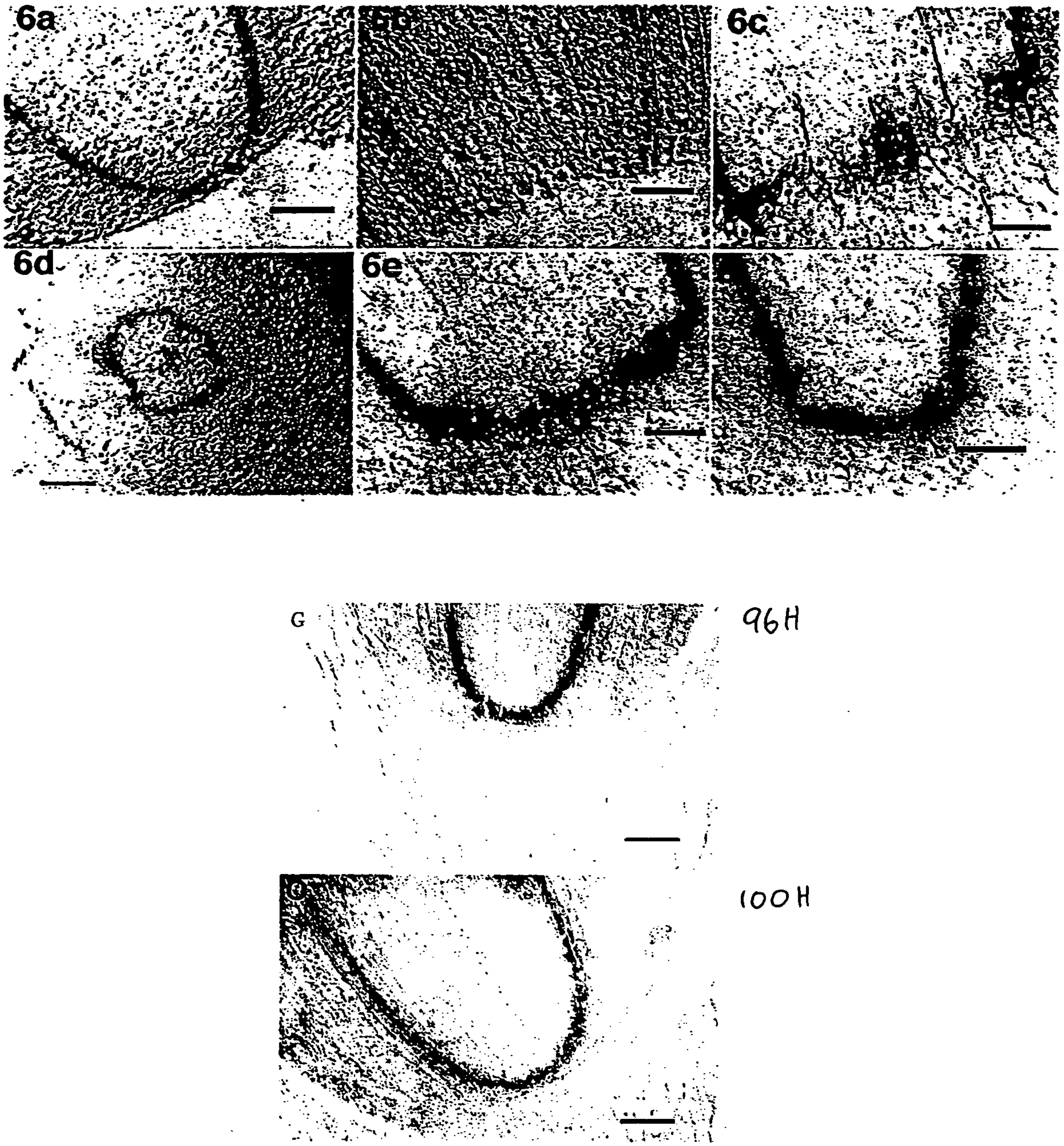


Fig. 27

Z25645

```
    ctttgtcaat ggtaaatgag ctgaggcaga tagtttctat ccaaggagac ccttctcaga
 61 gaatcgcagc ttacatggtg gaaggtctag ctgcaagaat ggccgcttca ggaaaattca
121 tctacagagc attgaaatgc aaagagcctc cttcggatga gaggcttgca gctatgagat
181 cctgtttgaa gtctgccctt gtttcaagtt cgggttttta gcagctaatg gtgcgatact
241 tgaagcaatc aaaggtgaag aagaagttca cataatcgat ttcgatataa accaagggaa
301 ccaatacatg acactgatac gaagcattgc tgagttngcc tgggtaaacg acctcgcctg
361 aggttaaaca ggaattgatg accctgaatc cagtnccaac cgctccattt gggggggcct
421 aaagaa
```

Fig. 28A

Z34183

```
    gagtacgatc ttaaagctat tcccggtgac gcgattctca atcagttcgc tatcgattcg
 61 gcttcttcgt ctaaccaagg cggcggagga gatacgtata ctacaaacaa gcggttgaaa
121 tgctcaaacg gcgtcgtgga aaccactaca gcgacggctg agatcaactc ggcatgttgt
181 cctggttgac tcgcaggaga acggtgtgcg tctcgttcac gcgcttttgg cttgcgctga
241 aagctgttca gaaagagaat ctgactgtag cggantctgg tgaagcaaat cggattctta
301 gccgtttctc aaatcggagc gatgagaaaa gtcgctactt act
```

Fig. 28B

Z34599

```
    aaatttttca attacctaat ataatgaaag ataagatctt aacaagtgac aaagggaaaa
 61 acagtaggat ttagtttggc ttcggtcgga aatctatcat cataaccggt tcaacagatc
121 aattcattga gccaccatct aattggtgag agtttccaag ccgaggtggc tatgagcggt
181 cgtgtgtgcc aacccaacat gagacagccg tcactctcct ccacccgata accctcaccg
241 ccgttgaaca gagccaaaag catactcgct tgcttaaacg cattcgaacc aatatgtgca
301 gccgcaaacc cagcagaccc gaaccggttc ctccantgac ttcaacgttt catgacggtt
361 caacttcggt ca
```

Fig. 28C

Z33772

```
    ttttttttta agtgagaacc ttaacaaatt taaccatttg aactgaaata tgaacatgta
 61 aagactcatt cacacttagc aaataggttt agaaccaaaa ctctaattat ttttatataa
121 tagggaaaaa aaagaaagaa aaattcttcc ataagtgtta gattagcttt tagtacctgt
181 gatcacccct aacctctggt aataatacat ggagatgatt taaccagtta cacaataacc
241 caagattaca gtaaaaacat aattatgttt tatgaaacat aaagactata tgctcttgtc
301 acttatctta cctccaagct gaagcaacgg attaagcttt tctcctccca gcaaaaatgg
361 gagctcaccc atttcttctt taaggttgta cttnttgca
```

Fig. 28D

Z37192

```
    gctatggaag gagagaagat ggttcatgtg attgatctcg atgcttctga gccagctcaa
 61 tggcttgctt tgcttcaagc ttttaactct aggcctgaag gtccacctca tttgagaatc
121 actggtgttc atcaccagaa ggaagtgctt gaacaaatgg ctcatagact cattgaggaa
181 gcagagaaac tcgatatccc gtttcagttt aatcccgttg tgagtaggtt agactgttta
241 aatgtagnac agtttagggt ttaaacagga gaggcnttag ccgttagctc ggttcttcaa
301 ttgcata
```

Fig. 28E

Z37191

```
    ccgatcatca aattagttat cttcagctca aattggattt ggtttggtat tacacccaca
 61 ccagaccaaa ttgaaccaac acacaaaggc tttacatgca gaggcagtag aagcatttaa
121 gccaaaatag cataaagaga cagaaagtca ccatcacaaa acaactaaga ttgtgtcccc
181 atgtatacaa aaaagaaagg gactctgctc ataaccaaaa tagaagacaa actgtaatat
241 atcattcact tcctgcatct ccaagctgat accgagtata gaggtcgatc ttgccagcaa
301 attactgcgc acccgntctc ttccttgatt ctatacccat caaaa
```

Fig. 28F

Z46550

```
   gtggaattac aattacagca atttgtattc aattgttgaa tctaagcctg gcttcatctc
 61 tttggcctgg aacgatttac ctctcctcac tctttcttcc tggcgataac caaaccaaac
121 cgatccggta ttcttagttt tgttttgttt tcaatgttat ttttggttag acaaatattc
181 aattgttaat atactccgtg gtcagagtgt tttgtttttc ttttagttcg aacgttgaat
241 taattcaggg gtaggttttg aattctctga accttatgtg ttttttggta acatcatttg
301 gatttgtgaa ctaggtttaa aaactggtct tagtcttgtt gttttctcat tagataattt
361 aaactggttt gcttctttat ttttgggttg ggataaaagt gaccgg
```

Fig. 28G

Z38048

```
   gtggaattnc aattacagca atttgtattc aattgttgaa tctaagcctg gcttcatctc
 61 tttggcctgg aacgatttac ctctcctcac tctttcttcc angcgataac caaaccaaac
121 cgatgccggt attcttagtt ttgttttgtt ttcaatgtta tttttggtta gacaaatatt
181 caattgttaa tatactccgt ggtcagagtg ttttgttttn cttttagttc gaacgttgaa
241 ttaattcagg ggtaggtttt gaattctctg aacctnatgt gttttntggt aacatcattt
301 ggatttgtga actaggttta aaaactggnc ttagtcttgt tgttttctca ttaggataat
361 ttaaactggt ttgcttcttt attttnggtt gggataaagt gaccgg
```

Fig. 28H

Z38085

```
    caaaactaca tttcatcact tttttgagca aaattacaaa taaaagagta gttacaaata
 61 tatttggctt tcaacttcct aattttatga aatagtaatt acatctcaaa cagatgacca
121 gaaccggtca ctttatccaa ccaaaaataa agaagcaaac cagtttaaat tatctaatga
181 gaaaacaaca agactaagac cagtttttaa acctagttca caaatccaaa tgatgttacc
241 aaaaaacaca taaggttcag agaattcaaa acctacccct ganttaattc aacgttcgaa
301 ctaaaagaaa aacaaaacac tctgaccacg gagtatatta acatttgatt atttgtctaa
361 ccaaaaataa cattgaaaac aaaacaaaac tanggaatac cggatcggt
```

Fig. 28I

F13896

```
    cccaacgggt cctgagcttc ttacttatat gcatatcttg tatgaagcct gcccttattt
 61 caaattcggt tatgaatctg ctaatggagc tatagctgaa gctgtgaaga acgaaagttt
121 tgtgcacatt atcgatttcc agatttctca aggtggtcaa tgggtgagtt tgatccgtgc
181 tcttggtgct agacctggtg gacctccgaa cgttaggata acgggaattg atgatccgag
241 atcatcgttt gctcgtcaag gaggacttgc agttagttgc acaaagcact tggca
```

Fig. 28J

F13897

```
    gggtcatcaa catatcactt actactacaa catttgacaa cttgttcctn cggatcatgc
 61 atgagtttta cttttacaaa cagattctgc aaactttaaa agcaagtttc taatctcttc
121 tgaaaccgaa caaggttttt attagttacc tccaagcaca agaagtgata agaggttgat
181 tcttccatcc taaatacaat gctccatctc tttcttcaag tgtatacttc tctgaataac
241 tctcaagcaa tcctttgatt gttgcgttca catacgagct caaaggatac ggtttaaatc
301 ccgccatgtg aaaccgaga
```

Fig. 28K

F13949

```
    caaaaattta tatatttgtg tgaacttaaa tttaaaaatc catcgcactg agcaaaataa
 61 nntcagaaac taaaaatttg tcatttaaga taaattgaat taaggaaaat atttttttaa
121 taattgaaac tccggtggaa atcaggagga gcgacatctc catgctgaaa ctccgacgag
181 ttctgtcctt tgccaacata ggagaagtga gttatgtttc tcctcgacgt gaaagcctct
241 cactggcgtc cgttggntna aacactcggc ttgagactcc gtgaagttac tgtgcgtcac
301 cggtgagaaa cccatctgta gaaacatcgc ttgccacgtc atcatcggcc tttctatcgg
361 acggctacga tccaacacca gcttctctat ctccggctgt ataaggaaa
```

Fig. 28L

T22782

```
    ctattttnac aatttatttt gttattagaa gtggtagtgg agtgaaaaaa caaatcctaa
 61 gcagtcctaa ccgatccccg aagctaaaga ttctncacct tcccaaataa agcaaaacct
121 agatccgaca ttgaaggaaa aacctttag atccatctct gaaaaaaacc aaccatgaag
181 agagatcatc atcatcatca tcatcaagat aagaagacta tgatgatgaa tgaagaagnc
241 gacggtaacg gcatggatga gcttctagct gttcttggtt ataaggttag gtcatccgaa
301 atggctgatg tttgctcaga aactcgagca gcttgaagtt atgatgtcta atgttcaagn
361 aagncggtct ttntcaactt cgcnacttnn gactgttcac tntaatncgg cggnngtttt
421 caacgntggc ttgntttcna tgntnaccga ccttaat
```

Fig. 28M

T21627

```
    atgggaaagg agcatttaat ctcgactcaa ttgctctacg agctctctcc ttgtttcaaa
 61 ctcggtttcg aggccgcgaa tctcgccatt ntcgacgccg ccgataacaa cgacggtgga
121 atnatgatac cgcacgtaat cgatttcaat atcggagaag gtggacaata cgttaacctt
181 ctccntacat tatccacgcg ccggaatggt aaaagtnaga gtcagaattc tccggtggtt
241 aanatcaccc gccgtggcga acaacgttta cgggatgttt agtcggatga cgggtggnga
301 agagaggttt aaaagcccgt ncgngntttt ttttgnagcc actncngntn atccg
```

Fig. 28N

H76979

```
    actcggtatc tccgtaagtt tcaacgtggt gacgagttta cgactcggtg atctgaatcg
 61 tnaatctntc gggtgtnatc ccgacgagac tttggctgta aacttagctt tcaagcttta
121 tcgtgttccc gacgaaagcg tatncacgga gaatccaaga cgaacttctc cggcgcgtga
181 agggacttaa accgcgcgtg gttactctag tggagcaaga aatgaattcg aatacggcgc
241 cgtttttagg gagagtaagt nagtcatgcg cgtttnacgg tgcgttnctt gantcggtcg
301 agtctacggt tcctagtacg gatttccgac ccgtgccaaa atttnnggaa ggaatttgcc
361 cgnaannttn naaaccgggt g
```

Fig. 28O

N96767

```
    atnaaaagtc ttttttttt ctttgttaca taagattcct acacttttcg aaatggaaaa
 61 tcacaatgat aataatatca gaataatctc gaaaattaat aataatatgg taataataag
121 aagaaaaaaa aagagtgtgt gaagttaacg ccaagcggat gcgacagtga gtgcccgtcc
181 catccaacca aagcacacac ctccgttatc ttctttaacg gtaaagcccg ggtggactcg
241 gtttccacga ctcttcatcg actccgctat cttctcactc aatggcatta actcaaaccc
301 agccatgctc atccgcattc gccatttncc ggaacanctc gnaccgctct atacgntcga
361 ttccttcgga cggcaccgng ttttactagc ttccggncaa ttccttcctn aactttggaa
421 cggtnggatt cgttcttggg accgtaggct tggcccgctt aagaacgnac cgtacagggg
481 nntgttttnt taatttccct taaaaggggg cgntttggg ttnatttttn ana
```

Fig. 28P

T43670

```
    caaccntttt atagtcaagc agctctcaac gctttttttt caaggtctgt naagcctcga
 61 aattatcaga ntttncaatc tccgtcgccg atgattganc tcacgtcggt gaatgatatg
121 agtttntttg gnggttctgg ttcatctcag cnttacggtt taccggttcc caggtctcan
181 acgcaacagc aacaatcgga ttacggttta tttggtggga tccgaatggg aatcgggtcg
241 ggtattaata attatccaac attaaccggc gttccgtgta ttgaaccggt tcaaaaccgg
301 gttcatgaat cggaggacca ttgttganta agnttaagag agctttgtng aaacaanctt
361 tttangattg atnaccg
```

Fig. 28Q

T76186

```
    tgcatacaac gcaccgtttt tcgtaacacg gtttcgcgaa gtctatttca tttctcctcg
 61 atttttgaca tgcttgagac aattgtgcca cgagaagacg aagagaggat gttccttgag
121 atggaggtct ttgggagaga ggcactgaat gtaattgctt gcnaaggttg ggaaagagtg
181 gagaggcctg agacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aaggattttg tgatcggtca aagataaccg ggtggctctt tcaaggntgg aaggggaagg
361 anctgtcatg ggtctttctt ttttggaaac cagagtccca aggttttncc ggaaaatcct
421 ccttgggnat ttnangnccc ttttttgtt tttttncccn gnnanttccc nggggnagtt
481 tccagtttna ggngngtttt tncnaaaa
```

Fig. 28R

T44774

```
    tgcatacaac gcaccgtttt tngtaacacg gtttcgcgaa gtctatttna tttctcctcg
 61 atttttgaca tgcttganac aattgtncca cgagaagacg aagagaggat gttccttgan
121 atggaggtct ttgggagana ggcactgaat gtaattnctt gcnaaggttg ggaaagagtg
181 gagaggcctg anacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aagggttttt tgatccntcc aagataaccg gtggctcttn caaagctttg aagggaagga
361 cctttcatgg gtcttttctt ttttggaacc aggtcccaag gttttncccg gaatccccgn
421 tggaattttg nnnccccttt tgatttttt tccccggnaa ttnccc
```

Fig. 28S

T45793

```
    gagacggtag atccgncgcg ctaaagcttc ggcgaagtaa gtagccactt tnntnatagc
 61 tccggcttga nacacagcta agcatccnat ttgcttcaca agagcttccg ctagagtcaa
121 attgtnctnc tggattgctt ctgcacaagc cataagcgcg tggactaaac gaacaccgtt
181 ctcttgcgag tnaaccagga taacagaacg anttgactca gccgccgccg tcgttgtcgt
241 ggtggttgtc gtcaccgtcg ttcctatgac tccaccaatn tgggtacccg tcgaagtcga
301 tgtaaccata ggatcagggc ttcgngcatg nttttaaaac gg
```

Fig. 28T

T46205

```
    gtttgattcg ttggaaggag ttccgaatag tcaagacaaa gtcatntctg aagtttactt
 61 agggaaacag atttgtaatc nggtggcttg tnaagntcct gacagagtcg agagacacga
121 aacgttgagt caatngggaa accggtttgg ttcgtccggt ttagcgccgg cacatcttgg
181 gtctaacgcg tttaagcaag cnagtatnct tttntntgtn tttaatagtg gccaaggtta
241 tcgtgtggag gagagtaatg gatgtttgat gttgggttgg cacactnngc ccactcattt
301 accacctccg gttttggaaa c
```

Fig. 28U

N96653

```
    taaaaattga tcccaaaaag gcataaatta aaaatgacct accaaaacga tatatataag
 61 aattttaaac aagtgaacga aaataaataa aataaacaaa aggcaaaacg gttcgattca
121 gttcggttta ggtcttggtc cgaacatatg tcatcaccgg tccactgatc tcaatctcaa
181 attcactcgn ctcgactcca ccaccgtcgt atgcttcgag tcaaactcag tacgncgccg
241 tcgagagttt ccaagcggag gtggtaatga gtggacgagt gtgccaaccc ancatcaaac
301 atccattact ttcctccaca cgntaacctt ggccactatt taaacacagg caaaangcat
361 acttgtttgc ttaaaccgcg ttagnccnaa gntttgccgg gcgntaaacc cggcngaccc
421 aanccggntt tcccnatttg ctcaaacggt ttngtgnctt ttggcttttt gnatggcctt
481 taaangnncc
```

Fig. 28V

T76483

aaaaaatggg aaaccatcac tcttgatgaa cttatgatca atccaggaga gacaacggtc
61 gtcaacngca ttcatcggtt acaatacacn cctgatgaaa ctgtgtcatt agactctcca
121 agagacacgg ttctgaagct attcagagat atcaatcctg acctctttgt gtttgcagag
181 attaacggaa tgtacaactc tcctttcttc atgacgaggt tccgagaagc gcttttncat
241 tacncttcac tctttgacat gtttgacacc acaatacacg gagaggatga gtacaaaaac
301 aggtcactgt ttggagagag agttactttt gaganacgcg nttgagcgtg attttcctgc
361 nngggnttca nancgggttt tnngggcctt aaaacctnca agaaatnggn ggtttgggtt
421 tt

Fig. 28W

F15454

aatcaatgtt ttggttatat ttcattacta gcaacccacc cacaaccaca tgacaattta
61 caagagaaaa acaaccacca ggtttggttt gtatacatat ataacttagg ttgtgttaca
121 acttaaaaca tcattgcaca tcctaaaaat ttcagcgacc agaatgtgtt tttgattgtg
181 cctctttctt tatccacctc aagtaaccat cattcactat aacttaccca atct

Fig. 28X

N37425

```
    gcgaatgttg agatcttgga agcaatagct ggggaaacca gagtccacat tatcgatttt
 61 aagattgcac agggatcaca atacatgttt ttaattcagg agcttgcgaa acgccctggt
121 gggccgccgt tgctgcgtgt nacgggtgtg gatgattcan agtccaccta tgctcgtggg
181 ggaggactca gcttggtagg tgagaggctt gcaactttgg cgcagtcatg tggtgtcccg
241 tttnagtttc acgatgccat catgtctggg tgcaaggtgc agcgggaaca tctcgggttg
301 gaacctggct ttgctgttgt tgtgaacttc ccatatgtat tacaccacat gccagacgag
361 agcgtaagtt tttgaaaatc acagngacag gcttctgcat ctnatcaana gcctttcccc
421 aaactggtac tctagtaggc aagattcaac acaacacttg catcna
```

Fig. 28Y

W43803

```
    atgnaacata tagcaaaaga tcatgcaatg agtactatat ctcttaggct acactcttac
 61 acacgctatg tcacaagcat aatataacaa cattctagtg ttcaagaacc ctaactctga
121 acttaatcca ctcgtgttgg cgagagacta tcaacagaaa agccctacat aaatcccagt
181 cgcttagaac gtaaganaca acatctatga agacgaagga acccatagag atgaagcata
241 cacgattcta cctttccacc cttgaagtaa ccagttaccg ttttgatcaa catcgaagtt
301 tttatcgtac ccgttttcgg attttcaact tcagattctg catcagttcc ttctcaagcg
361 gnagctgtcc taaatccggg tcgggtcagt ctcggctggc actggttata tggctctggg
421 ctctccactc tctctggtct tcacaaggca cancattcac aatctntttt ccataaaact
481 nnttttcntn catnngncnn atnttggctt ccctnggntg gttggggnnc ncnt
```

Fig. 28Z

W43538

```
    tcaaggttct tctttgtcat cttgttgccg aatccacaaa gaggagaata aagattcgac
 61 ctttattaga tattaacgac tctggatttt tgggtttttg gagttggatc cacatgggtt
121 cttatccgga tggattccct ggatccatgg acgagttgga tttcaataag gactttgatt
181 tgcctccctc ctcaaaccaa accttaggtt tagctaatgg gttctattta gatgacttag
241 atttctcatc cttggatcct ccagaggcat atccctccca gaacaacanc aacaacatca
301 tcaacaacaa agctgtagca ggagatctgt tatcatcttc aactgaatga cgntggattc
361 tctgattctg ttttgagtat ataagccaag ttctnatggg agnnggtnat gnagagaagc
421 ctttgtatgt tcatgnngnt ttggtnatta agntgctngg aaannactcn ntnngc
```

Fig. 28AA

SCL 1

```
LSMVNELRQI VSIQGDPSQR IAAYMVEGLA ARMAASGKFI YRALKCKEPP
SDERLAAMQV LFEVCPCFKF GFLAANGAIL EAIKGEEEVH IIDFDINQGN
QYMTLIRSIA ELPGKRPRLR LTGIDDPESV QRSIGGLRII GLRLEQLAED
NGVSFKFKAM PSKTSIVSPS TLGCKPGETL IVNFAFQLHH MPDESVTTVN
QRDELLHMVK SLNPKLVTVV EQDVNTNTSP FFPRFIEAYE YYSAVFESLD
MTLPRESQER MNVERQCLAR DIVNIVACEG EERIERYEAA GKWRARMMMA
GFNPKPMSAK VTNNIQNLIK QQYCNKYKLK EEMGELHFCW EEKSLIVASA
WR*
```

Fig. 28AB

SCL 3

AMEGEKMVHV IDLDASEPAQ WLALLQAFNS RPEGPPHLRI TGVHHQKEVL

EQMAHRLIEE AEKLDIPFQF NPVVSRLDCL NVEQLRVKTG EALAVSSVLQ

LHTFLASDDD LMRKNCALRF HNNPSGVDLQ RVLMMSHGSA AEARENDMSN

NNGYSPSGDS ASSLPLPSSG RTDSFLNAIW GLSPKVMVVT EQDSDHNGST

LMERLLESLY TYAALFDCLE TKVPRTSQDR IKVEKMLFGE EIKNIISCEG

FERRERHEKL EKWSQRIDLA GFGNVPLSYY AMLQARRLLQ GCGFDGYRIK

EESGCAVICW QDRPLYSVSA WRCRK*

Fig. 28AC

SCL 5

GTSPTGPELL TYMHILYEAC PYFKFGYESA NGAIAEAVKN ESFVHIIDFQ

ISQGGQWVSL IRALGARPGG PPNVRITGID DPRSSFARQG GLELVGQRLG

KLAEMCGVPF EFHGAALFCT EVEIEKLGVR NGEALAVNFP LVLHHMPDES

VTVENHRDRL LRLVKHLSPN VVTLVEQEAN TNTAPFLPRF VETMNHYLAV

FESIDVKLAR DHKERINVEQ HCLAREVENL IACEGVEREE RHEPLGKWRS

RFHMAGFKPY PLSSYVNATI KGLLESYSEK YTLEERDGAL YLGWKNQPLI

TSCAWR*

Fig. 28AD

SCL 6

AAIFYGHHHH TPPPAKRLNP GPVGITEQLV KAAEVIESDT CLAQGILARL

NQQLSSPVGK PLERAAFYFK EALNNLLHNV SQTLNPYSLI FKIAAYKSFS

EISPVLQFAN FTSNQALLES FHGFHRLHII DFDIGYGGQW ASLMQELVLR

DNAAPLSLKI TVFASPANHD QLELGFTQDN LKHFASEINI SLDIQVLSLD

LLGSISWPNS SEKEAVAVNI SAASFSHLPL VLRFVKHLSP TIIVCSDRGC

ERTDLPFSQQ LAHSLHSHTA LFESLDAVNA NLDAMQKIER FLIQPEIEKL

VLDRSRPIER PMMTWQAMFL QMGFSPVTHS NFTESQAECL VQRTPVRGFH

VEKKHNSLLL CWQRTELVGV SAWRCRSS*

Fig. 28AE

SCL 11

KKWETITLDE LMINPGETTV VNCIHRLQYT PDETVSLDSP RDTVLKLFRD

INPDLFVFAE INGMYNSPFF MTRFREALFH YSSLFDMFDT TIHCERRDEV

ISCEGAERFA RPETYKQWRV RILRAGFKPA TISKQIMKEA KEIVRKRYHR

DFVIDSDNNW MLQGWKGRVI YAFSCWKPAE KFTNNNLNI*

Fig. 28AF

SCL 13

ANVEILEAIA GETRVHIIDF QIAQGSQYMF LIQELAKRPG GPPLLRVTGV

DDSQSTYARG GGLSLVGERL ATLAQSCGVP FEFHDAIMSG CKVQREHLGL

EPGFAVVVNF PYVLHHMPDE SVSVEKYRDR LLHLIKSLSP KLVTLVEQES

NTNTSPLVSR FVETLDYYTA MFESIDAARP RDDKQRISAE QHCVARDIVN

MIACEESERV ERHEVLGKWR VRMMMAGFTG WPVSTSAAFA ASEMLKAYDK

NYKLGGHEGA LYLFWKRRPM ATCSVWKPNP NYIG*

Fig. 28AG

SCL 14

LLKVLLCHLV AESTKRRIKI RPLLDINDSG FLGFWSWIHM GSYPDGFPGS
MDELDFNKDF DLPPSSNQTL GLANGFYLDD LDFSSLDPPE AYPSQNNNNN
NINNKAVAGD LLSSSSDDAD FSDSVLKYIS QVLMEEDMEE KPCMFHDALA
LQAAEKSLYE ALGEKDPSSS SASSVDHPER LASHSPDGSC SGGAFSDYAS
TTTTTSSDSH WSVDGLENRP SWLHTPMPSN FVFQSTSRSN SVTGGGGGN
SAVYGSGFGD DLVSNMFKDD ELAMQFKKGV EEASKFLPKS SQLFIDVDSY
IPMNSGSKEN GSEVFVKTEK KDETEHHHHH SYAPPPNRLT GKKSHWRDED
EDFVEERSNK QSAVYVEESE LSEMFDNMFL CGPGKPVCIL NQNFPTESAK
VVTAQSNGAK IRGKKSTSTS HSNDSKKETA DLRTLLVLCA QAVSVDDRRT
ANVXLRQIRE HSSPLGNGSE RLAHYFANSL EARLAGTGTQ IYTALSSKKT
SAADMLKAYQ TYMSVCPFKK AAIIFANHSM MRFTANANTI HIIDFGISYG
FQWPALIHRL SLSRPGGSPK LRITGIELPQ RGFRPAEEFR RQVIAWLDTV
SDTMFRLSTT QLLRNGETIQ VEDLKLRQGE YVVVNSLFRF RNLLDETVLV
NSPRDAVLKL IRKINPNVFI PAILSGNYNA PFFVTRFREA LFHYSAVFDM
CDSKLAREDE MRLMYVFEFY GREIVNVVAS EGTERVESRE TYKQWQARLI
RAGFRQLPLE KELMQNLKLK IENGYDKNFD VDQNGNWLLQ GWKGRIVYAS
SLWVPSSS*

Fig. 28AH

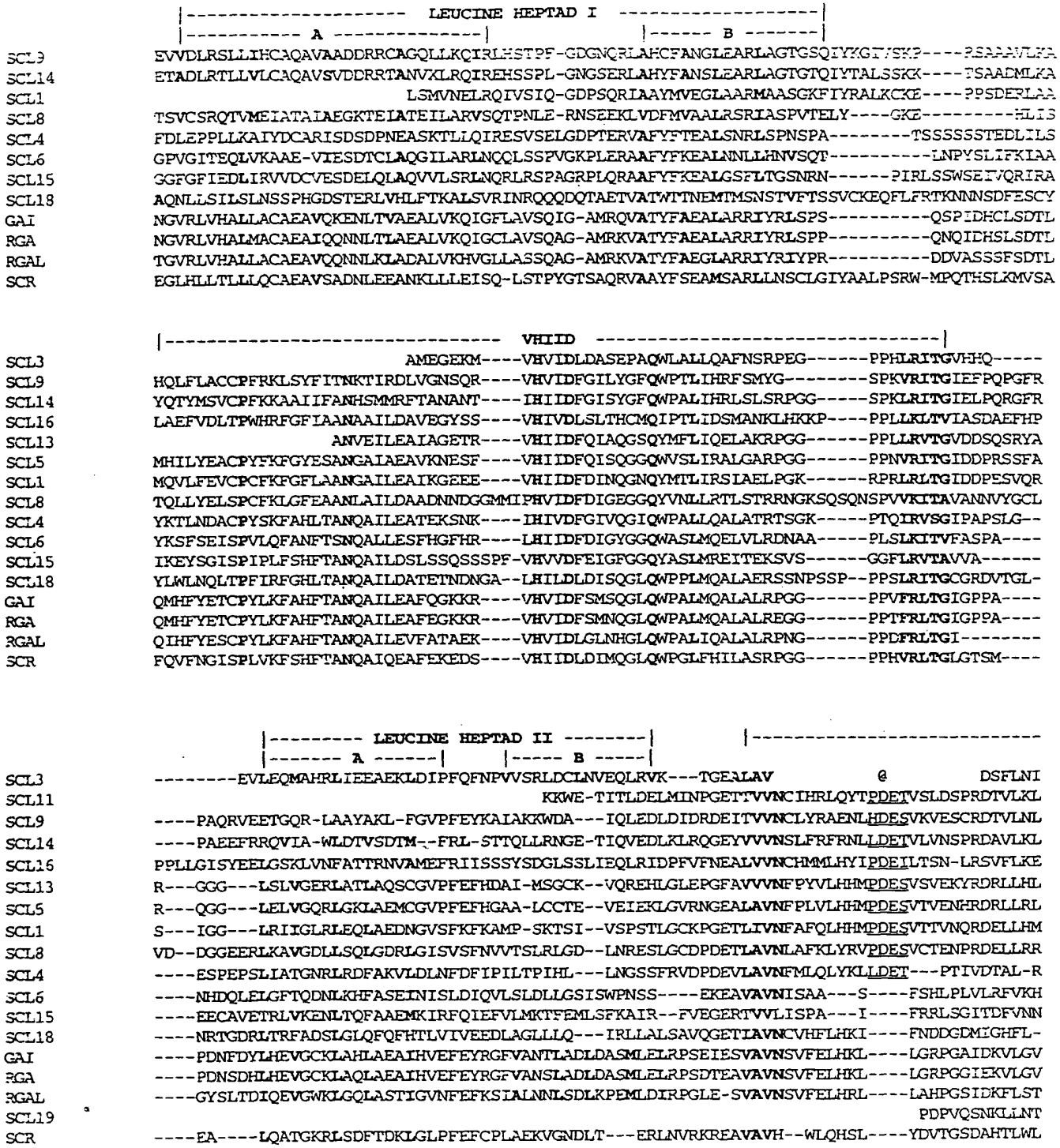

LEUCINE HEPTAD I
A
B
VHIID
LEUCINE HEPTAD II
A
B
SCL9
SCL14
SCL1
SCL8
SCL4
SCL6
SCL15
SCL18
GAI
RGA
RGAL
SCR
SCL3
SCL16
SCL13
SCL5
SCL11
SCL19

Fig. 29A

@SSVLQLHTFLASDDDLMRKNCALRFHNNPSGVDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLPLPSSGRT

Fig. 29B

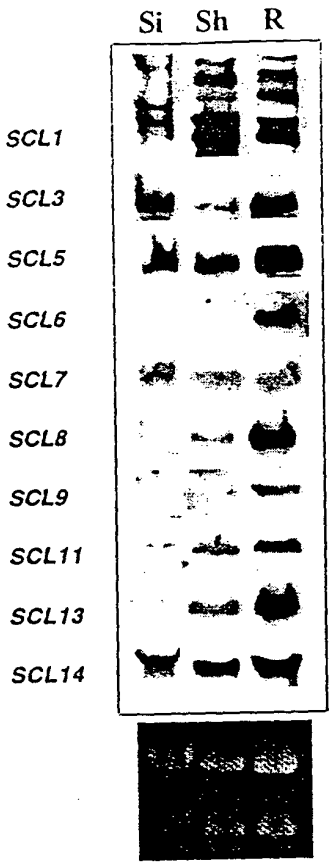


Fig. 30

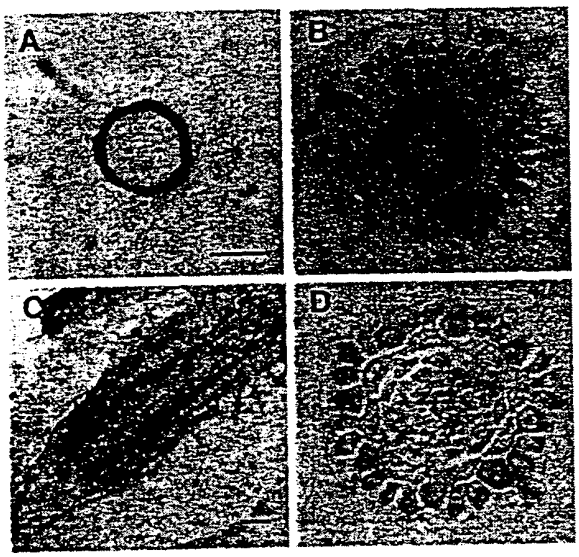
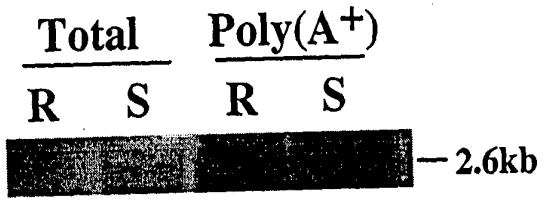


Fig. 31

RNA Blot Analysis



Either total RNA or poly (A^+) RNA was probed with the full length of cDNA.
About 2.6kb fragment was hybridized to the probe.
R: Roots, S: Shoots

Fig. 32

CBPBT44 partial cDNA sequence

GCGGCCGCGCAGAGCCGCCGCGTGGCGGTGGCGTTCCAGGCGTACAACGCGCTGTCGCCG
CTCGTCAAGTTCTCGCACTTCACGGCCAACCAGGCCATCCTGCAGGCGCTCGACGGCGAG
GACTGCCTCCACGTGATCGACCTGGACATCATGCAGGGCCTGCAGTGGCCGGGGCTCTTC
CACATCCTCGCGTCCCGCCCGCGCAAGCCGCGGTCGCTCCGGATCACCGGGCTCGGCGCG
TCGCTCGACGTCCTCGAGGCCACTGGCCGCCGCCTCGCCGACTTCGCGGCCTCGCTCGGC
CTCCCGTTCGAGTTCCGCCCCATCGAGGGGAAGATCGGGCACGTCGCCGACGCCGCGGCG
CTCCTCGGCTCGCGCCAGCGGCGGCGGGATGACGAGGCCACCGTGGTGCACTGGATGCAC
CACTGCCTCTATGACGTGACGGGGTCGGACGTGGGCACGGTGCGGCTGCTCCGGAGCCTG
CGCCCGAAGCTGATCACCATCGTGGAGCAGGACCTGGGCCACAGCGGCGATTTCCTGGGC
CGGTTCGTGGAGGCGCTGCACTACTACTCGGCGCTGTTCGACGCGCTGGGAGACGGCGCC
GGCGCGGCCGAGGAGGAGTCGGCCGAGCGGTACGCGGTTGAGCGACAGCTCCTGGGCGCG
GAGATACGCAACATCGTGGCCGTAGGGGGGCCCAAGCGGACAGGGGAGGTGCGCGTGGAG
CGGTGGAGCCACGAACTGCGGCACGCCGGGTTCCGGCCAGTGTCCCTGGCCGGGAGCCCT
GCCGCGCAGGCCAGGCTGCTCCTCGGCATGTATCCGTGGAAGGGGTACACGCTGGTGGAG
GAGGACGCGTGCCTTAAGCTGGGCTGGAAGGACCTCTCCCTGCTCACCGCGTCGGCGTGG
GAGCCGGCGGACGACGCTGCCGCTTCTGCGCCCACCGGTTAACGAGTACGAGCGGACGCG
TGGGTCGAC

CBPBT44 partial amino acid sequence

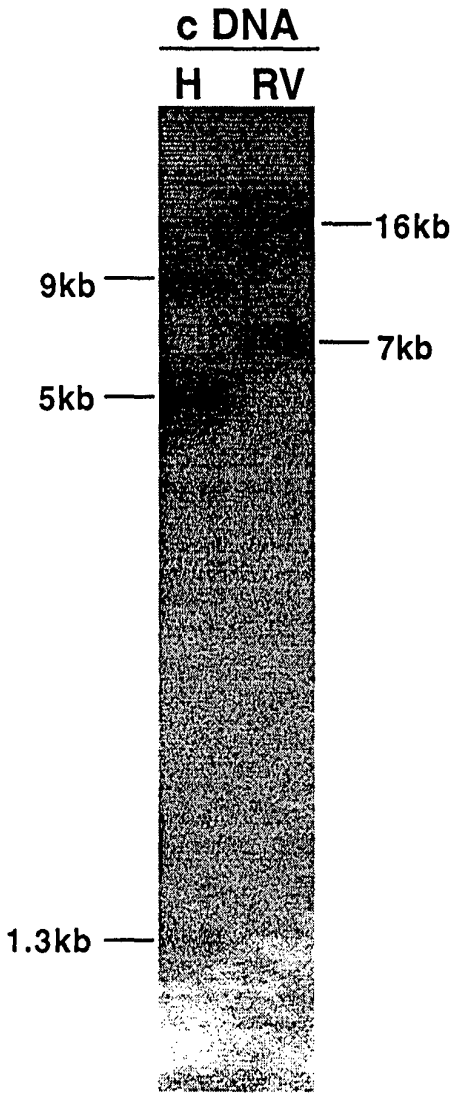
AAAQSRRVAVAFQAYNALSPLVKFSHFTANQAILQALDGEDCLHVIDLDIMQGLQWPGLF
HILASRPRKPRSLRITGLGASLDVLEATGRRLADFAASLGLPFEFRPIEGKIGHVADAAA
LLGSRQRRRDDEATVVHWMHHCLYDVTGSDVGTVRLLRSLRPKLITIVEQDLGHSGDFLG
RFVEALHYYSALFDALGDGAGAAEEESAERYAVERQLLGAEIRNIVAVGGPKRTGEVRVE
RWSHELRHAGFRPVSLAGSPAAQARLLLGMYPWKGYTLVEEDACLKLGWKDLSLLTASAW
EPADDAAASAPTGXRVRADAWVD

Fig. 33

```
Zm SCR                                                  GRVAAAFQVF NGISPFVKFS
CBPBT44                                                 RRVAVAFQAY NALSPLVKFS
At SCR                                                  LKMVSAFQVF NGISPLVKFS

Zm SCR    HFTANQAIQE AFEREERVHI IDLDIMQGLQ WPGLFHILAS RPGGPPRVRL
CBPBT44   HFTANQAILQ ALDGEDCLHV IDLDIMQGLQ WPGLFHILAS RPRKPRSLRI
At SCR    HFTANQAIQE AFEKEDSVHI IDLDIMQGLQ WPGLFHILAS RPGGPPHVRL

Zm SCR    TGLGASMEAL EATGKRLSDF ADTLGLPFEF CAVAEKAGNV DPEKLGVTRR
CBPBT44   TGLGASLDVL EATGRRLADF AASLGLPFEF RPIEGKIGHV ADAAALLGSR
At SCR    TGLGTSMEAL QATGKRLSDF TDKLGLPFEF CPLAEKVGNL DTERLNVRKR

Zm SCR    ------EAVA VHWLHHSLYD VTGSDSNTLW LIQRLAPKVV TMVEQDLSHS
CBPBT44   QRRRDDEATV VHWMHHCLYD VTGSDVGTVR LLRSLRPKLI TIVEQDLGHS
At SCR    ------EAVA VHWLQHSLYD VTGSDAHTLW LLQRLAPKVV TVVEQDLSHA

Zm SCR    GSFLARFVEA IHYYSALFDS LDASYGEDSP ERHV---VEQ QLLSREIRNV
CBPBT44   GDFLGRFVEA LHYYSALFDA LGDGAGAAEE ESAERYAVER QLLGAEIRNI
At SCR    GSFLGRFVEA IHYYSALFDS LGASYGEESE ERHV---VEQ QLLSKEIRNV

Zm SCR    LAVGGPARTG DVKFGSWREK LAQSGFRAAS LAGSAAAQAS LLLGMFPSDG
CBPBT44   VAVGGPKRTG EVRVERWSHE LRHAGFRPVS LAGSPAAQAR LLLGMYPWKG
At SCR    LAVGGPSRSG EVKFESWREK MQQCGFKGIS LAGNAATQAT LLLGMFPSDG

Zm SCR    YTLVEENGAL KLGWKDLCLL TASAWRPIQV PPCR
CBPBT44   YTLVEEDACL KLGWKDLSLL TASAWEPADD AAASAPTG
At SCR    YTLVDDNGTL KLGWKDLSLL TASAWTPRS
```


Fig. 34

DNA Blot Analysis



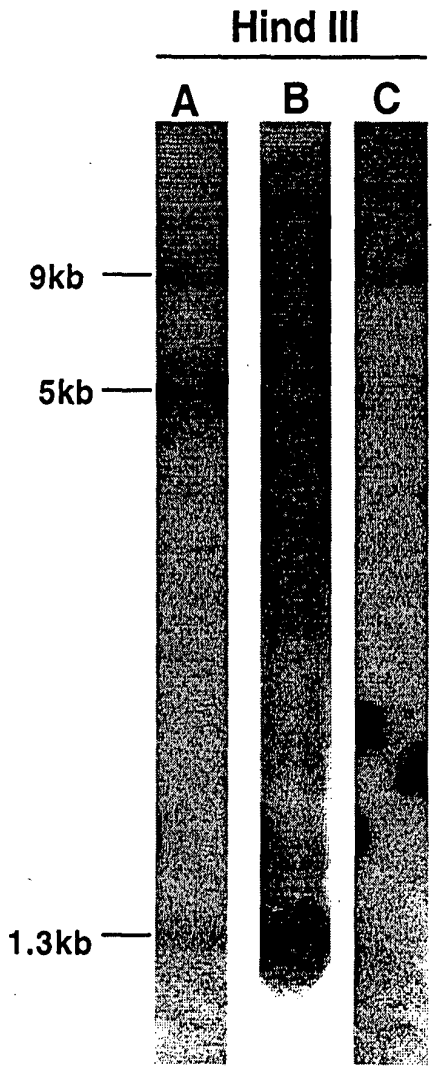


Fig. 35